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(54) Title: VERTEBRATE SMOOTHENED PROTEINS			
(57) Abstract Novel vertebrate homologues of Smoothened, including human and rat Smoothened, are provided. Compositions including vertebrate Smoothened chimeras, nucleic acid encoding vertebrate Smoothened, and antibodies to vertebrate Smoothened, are also provided.			

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Vertebrate Smoothened Proteins

FIELD OF THE INVENTION

The present invention relates generally to novel Smoothened proteins which interact with Hedgehog and Patched signalling molecules involved in cell proliferation and differentiation. In particular, the invention relates to newly identified and isolated vertebrate Smoothened proteins and DNA encoding the same, including rat and human Smoothened, and to various modified forms of these proteins, to vertebrate Smoothened antibodies, and to various uses thereof.

BACKGROUND OF THE INVENTION

Development of multicellular organisms depends, at least in part, on mechanisms which specify, direct or maintain positional information to pattern cells, tissues, or organs. Various secreted signalling molecules, such as members of the transforming growth factor-beta ("TGF-beta"), Wnt, fibroblast growth factor ("FGF"), and hedgehog families, have been associated with patterning activity of different cells and structures in *Drosophila* as well as in vertebrates [Perrimon, *Cell*, 80:517-520 (1995)].

Studies of *Drosophila* embryos have revealed that, at cellular blastoderm and later stages of development, information is maintained across cell borders by signal transduction pathways. Such pathways are believed to be initiated by extracellular signals like Wingless ("Wg") and Hedgehog ("Hh"). The extracellular signal, Hh, has been shown to control expression of TGF-beta, Wnt and FGF signalling molecules, and initiate both short-range and long-range signalling actions. A short-range action of Hh in *Drosophila*, for example, is found in the ventral epidermis, where Hh is associated with causing adjacent cells to maintain *wingless (wg)* expression [Perrimon, *Cell*, 76:781-784 (1984)]. In the vertebrate central nervous system, for example, Sonic hedgehog ("SHh"; a secreted vertebrate homologue of dHh) is expressed in notocord cells and is associated with inducing floor plate formation within the adjacent neural tube in a contact-dependent manner [Roelink et al., *Cell*, 76:761-775 (1994)]. Perrimon, *Cell*, 80:517-520 (1995) provide a general review of some of the long-range actions associated with Hh.

Studies of the Hh protein in *Drosophila* ("dHh") have shown that *hh* encodes a 46 kDa native protein that is cleaved into a 39 kDa form following signal sequence cleavage and subsequently cleaved into a 19 kDa amino-terminal form and a 26 kDa carboxy-terminal form [Lee et al., *Science*, 266:1528-1537 (1994)]. Lee et al. report that the 19 kDa and 26 kDa forms have different biochemical properties and are differentially distributed. DiNardo et al. and others have disclosed that the dHh protein triggers a signal transduction cascade that activates *wg* [DiNardo et al., *Nature*, 332:604-609 (1988); Hidalgo and Ingham, *Development*, 110:291-301 (1990); Ingham and Hidalgo, *Development*, 117:283-291 (1993)] and at least another segment polarity gene, *patched (ptc)* [Hidalgo and Ingham, *supra*; Tabata and Kornberg, *Cell*, 76:89-102 (1994)]. Properties and characteristics of dHh are also described in reviews by Ingham et al., *Curr. Opin. Genet. Dev.*, 5:492-498 (1995) and Lumsden and Graham et al., *Curr. Biol.*, 5:1347-1350 (1995). Properties and characteristics of the vertebrate homologue of dHh, Sonic hedgehog, are described by Echelard et al., *Cell*, 75:1417-1430 (1993); Krauss et al., *Cell*, 75:1431-1444 (1993); Riddle et al., *Cell*, 75:1401-1416 (1993); Johnson et al., *Cell*, 79:1165-1173 (1994); Fan et al., *Cell*, 81:457-465 (1995); Roberts et al., *Development*, 121:3163-3174 (1995); and Hynes et al., *Cell*, 80:95-101 (1995).

In Perrimon, *Cell*, 80:517-520 (1995), it was reported that the biochemical mechanisms and receptors by which signalling molecules like Wg and Hh regulate the activities, transcription, or both, of secondary signal transducers have generally not been well understood. In *Drosophila*, genetic evidence indicates that Frizzled ("Fz") functions to transmit and transduce polarity signals in epidermal cells during hair and bristle development. Fz rat homologues which have structural similarity with members of the G-protein-coupled receptor superfamily have been described by Chan et al., *J. Biol. Chem.*, 267:25202-25207 (1992). Specifically, Chan et al. describe isolating two different cDNAs from a rat cell library, the first cDNA encoding a predicted 641 residue protein, Fz-1, having 46% homology with *Drosophila* Fz, and a second cDNA encoding a protein, Fz-2, of 570 amino acids that is 80% homologous with Fz-1. Chan et al. state that mammalian fz may constitute a gene family important for transduction and intercellular transmission of polarity information during tissue morphogenesis or in differentiated tissues. Recently, Bhanot et al. did describe the identification of a *Drosophila* gene, *frizzled2* (*Dfz2*), and predicted Dfz2 protein, which can function as a Wg receptor in cultured cells [Bhanot et al., *Nature*, 382:225-230 (1996)]. Bhanot et al. disclose, however, that there is no *in vivo* evidence that shows Dfz2 is required for Wg signalling.

Although some evidence suggests that cellular responses to dHh are dependent on the transmembrane protein, *smoothed* (*dSmo*), [Nusslein-Volhard et al., *Wilhelm Roux's Arch. Dev. Biol.*, 193:267-282 (1984); Jurgens et al., *Wilhelm Roux's Arch. Dev. Biol.*, 193:283-295 (1984); Alcedo et al., *Cell*, 86:221-232 (July 26, 1996); van den Heuvel and Ingham, *Nature*, 382:547-551 (August 8, 1996)], and are negatively regulated by the transmembrane protein, "Patched" [(Hooper and Scott, *Cell*, 59:751-765 (1989); Nakano et al., *Nature*, 341:508-513 (1989); Hidalgo and Ingham, *supra*; Ingham et al., *Nature*, 353:184-187 (1991)], the receptors for Hh proteins have not previously been biochemically characterized. Various gene products, including the Patched protein, the transcription factor cubitus interruptus, the serine/threonine kinase "fused", and the gene products of *Costal-2*, *smoothed* (*smo*) and *Suppressor of fused* (*Su(fu)*), have been implicated as putative components of the Hh signalling pathway.

Prior studies in *Drosophila* led to the hypothesis that *ptc* encoded the Hh receptor [Ingham et al., *Nature*, 353:184-187 (1991)]. The activity of the *ptc* product, which is a multiple membrane spanning cell surface protein referred to as Patched [Hooper and Scott, *supra*], represses the *wg* and *ptc* genes and is antagonized by the Hh signal. Patched was proposed by Ingham et al. to be a constitutively active receptor which is inactivated by binding of Hh, thereby permitting transcription of Hh-responsive genes. As reported by Bejsovec and Wieschaus, *Development*, 119:501-517 (1993), however, Hh has effects in *ptc* null *Drosophila* embryos and thus cannot be the only Hh receptor. Accordingly, the role of Patched in Hh signalling has not been fully understood.

Goodrich et al. have isolated a murine *patched* gene [Goodrich et al., *Genes Dev.*, 10:301-312 (1996)]. Human *patched* homologues have also been described in recently published literature. For instance, Hahn et al., *Cell*, 85:841-851 (1996) describe isolation of a human homologue of *Drosophila ptc*. The gene displays up to 67% sequence identity at the nucleotide level and 60% similarity at the amino acid level with the *Drosophila* gene [Hahn et al., *supra*]. Johnson et al. also provide a predicted amino acid sequence of a human Patched protein [Johnson et al., *Science*, 272:1668-1671 (1996)]. Johnson et al. disclose that the 1447 amino acid protein has 96% and 40% identity to mouse and *Drosophila* Patched, respectively. The human and

mouse data from these investigators suggest that *patched* is a single copy gene in mammals. According to Hahn et al., Cell, 85:841-851 (1996), analyses revealed the presence of three different 5' ends for their human *ptc* gene. Hahn et al. postulate there may be at least three different forms of the Patched protein in mammalian cells: the ancestral form represented by the murine sequence, and the two human forms. Patched is further discussed in a recent review by Marigo et al., Development, 122:1225 (1996).

Studies in *Drosophila* have also led to the hypothesis that Smo could be a candidate receptor for Hh [Alcedo et al., supra; van den Heuvel and Ingham, supra]. The *smoothened* (*smo*) gene was identified as a segment polarity gene and initially named *smooth* [Nusslein-Volhard et al., supra]. Since that name already described another locus, though, the segment polarity gene was renamed *smoothened* [Lindsley and Zimm, "The Genome of *Drosophila melanogaster*," San Diego, CA:Academic Press (1992)]. As first reported by Nusslein-Volhard et al., supra, the *smo* gene is required for the maintenance of segmentation in *Drosophila* embryos.

Alcedo et al., supra, have recently described the cloning of the *Drosophila smoothened* gene [see also, van den Heuvel and Ingham, supra]. Alcedo et al. report that hydropathy analysis predicts that the putative Smo protein is an integral membrane protein with seven membrane spanning alpha helices, a hydrophobic segment near the N-terminus, and a hydrophilic C-terminal tail. Thus, Smo may belong to the serpentine receptor family, whose members are all coupled to G proteins. Alcedo et al., supra, also report that *smo* is necessary for Hh signalling and that it acts downstream of *hh* and *ptc*.

As discussed in Pennisi, Science, 272:1583-1584 (1996), certain development genes are believed to play some role in cancer because they control cell growth and specialization. Recent studies suggest that *patched* is a tumor suppressor, or a gene whose loss or inactivation contributes to the excessive growth of cancer cells. Specifically, Hahn et al. and other investigators have found that *patched* is mutated in some common forms of basal cell carcinomas in humans [Hahn et al., Cell, 85:841-851 (1996); Johnson et al., supra; Gailani et al., in Letters, Nature Genetics, 13:September, 1996]. Hahn et al. report that alterations predicted to inactivate the *patched* gene product were found in six unrelated patients having basal cell nevus syndrome ("BCNS"), a familial complex of cancers and developmental abnormalities. Hahn et al. also report that the *ptc* pathway has been implicated in tumorigenesis by the cloning of the pancreatic tumor suppressor gene, *DPC4*. Vertebrate homologues of two other *Drosophila* segment polarity genes, the murine mammary *Wnt1* [Rijsewijk et al., Cell, 50:649 (1987)] and the human glioblastoma *GLI* [Kinzler et al., Science, 236:70 (1987)], have also been implicated in cancer.

SUMMARY OF THE INVENTION

Applicants have identified cDNA clones that encode novel vertebrate Smoothened proteins, designated herein as "vSmo." In particular, cDNA clones encoding rat Smoothened and human Smoothened have been identified. The vSmo proteins of the invention have surprisingly been found to be co-expressed with Patched proteins and to form physical complexes with Patched. Applicants also discovered that the vSmo alone did not bind Sonic hedgehog but that vertebrate Patched homologues did bind Sonic hedgehog with relatively high affinity. It is believed that Sonic hedgehog may mediate its biological activities through a multi-subunit receptor in which vSmo is a signalling component and Patched is a ligand binding component, as well as a ligand regulated suppressor of vSmo. Accordingly, without being limited to any one theory, pathological

conditions, such as basal cell carcinoma, associated with inactivated (or mutated) Patched may be the result of constitutive activity of vSmo or vSmo signalling following from negative regulation by Patched.

In one embodiment, the invention provides isolated vertebrate Smoothened. In particular, the invention provides isolated native sequence vertebrate Smoothened, which in one embodiment, includes an amino acid sequence comprising residues 1 to 793 of Figure 1 (SEQ ID NO:2). The invention also provides isolated native sequence vertebrate Smoothened which includes an amino acid sequence comprising residues 1 to 787 of Figure 4 (SEQ ID NO:4). In other embodiments, the isolated vertebrate Smoothened comprises at least about 80% identity with native sequence vertebrate Smoothened comprising residues 1 to 787 of Figure 4 (SEQ ID NO:4).

In another embodiment, the invention provides chimeric molecules comprising vertebrate Smoothened fused to a heterologous polypeptide or amino acid sequence. An example of such a chimeric molecule comprises a vertebrate Smoothened fused to an epitope tag sequence.

In another embodiment, the invention provides an isolated nucleic acid molecule encoding vertebrate Smoothened. In one aspect, the nucleic acid molecule is RNA or DNA that encodes a vertebrate Smoothened, or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under stringent conditions. In one embodiment, the nucleic acid sequence is selected from:

- (a) the coding region of the nucleic acid sequence of Figure 1 (SEQ ID NO:1) that codes for residue 1 to residue 793 (i.e., nucleotides 450-452 through 2826-2828), inclusive;
- (b) the coding region of the nucleic acid sequence of Figure 4 (SEQ ID NO:3) that codes for residue 1 to residue 787 (i.e., nucleotides 13-15 through 2371-2373), inclusive; or
- (c) a sequence corresponding to the sequence of (a) or (b) within the scope of degeneracy of the genetic code.

In a further embodiment, the invention provides a vector comprising the nucleic acid molecule encoding the vertebrate Smoothened. A host cell comprising the vector or the nucleic acid molecule is also provided. A method of producing vertebrate Smoothened is further provided.

In another embodiment, the invention provides an antibody which specifically binds to vertebrate Smoothened. The antibody may be an agonistic, antagonistic or neutralizing antibody.

In another embodiment, the invention provides non-human, transgenic or knock-out animals.

Another embodiment of the invention provides articles of manufacture and kits that include vertebrate Smoothened or vertebrate Smoothened antibodies.

A further embodiment of the invention provides protein complexes comprising vertebrate Smoothened protein and vertebrate Patched protein. In one embodiment the complexes further include vertebrate Hedgehog protein. The invention also provides vertebrate Patched which binds to vertebrate Smoothened. Optionally, the vertebrate Patched comprises a sequence which is a derivative of or fragment of a native sequence vertebrate Patched.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the nucleotide (SEQ ID NO:1) and deduced amino acid sequence (SEQ ID NO:2) of native sequence rat Smoothened.

Figure 2 shows the primary structure of rat Smo (rSmo) and Drosophila Smo (dsmo). The signal peptide sequences are underlined, conserved amino acids are boxed, cysteines are marked with asterisks, potential glycosylation sites are marked with dashed boxes, and the seven hydrophobic transmembrane domains are shaded.

5 Figure 3 shows tissue distribution of SHH, Smo and Patched in embryonic and adult rat tissues. *In situ* hybridization of SHH (left column): Smo (middle column) and Patched (right column, not including insets) to rat tissues. Row E15 Sag, sagittal sections through E15 rat embryos. Rows E9, E10, E12, and E15, coronal sections through E9 neural folds, E10 neural tube and somites, E12 and E15 neural tube. Insets in Row E12 show sections through forelimb bud of E12 rat embryos. Legend- ht=heart; sk=skin;
10 bl=bladder; ts=testes; lu=lung; to=tongue; vtc=vertebral column; nf=neural fold; nc=notocord; so=somite; fp=floor plate; vh=ventral horn; vz=ventricular zone; cm=cardiac mesoderm and vm=ventral midbrain.

Figure 4 shows the nucleotide (SEQ ID NO:3) and deduced amino acid sequence (SEQ ID NO:4) for native sequence human Smoothened.

15 Figure 5 shows the primary structure of human Smo (hSmo) and rat Smo (rat.Smo) and homology to Drosophila Smo (dros.smo). Conserved amino acids are boxed.

Figure 6 illustrates the results of binding and co-immunoprecipitation assays which show SHH-N binds to mPatched but not to rSmo. Staining of cells expressing the Flag tagged rSmo (a and b) or Myc tagged mPatched (c, d, and e) with (a) Flag (Smo) antibody; (c) Myc (mPatched) antibody; (b and d) IgG-SHH-N; or (e) Flag tagged SHH-N. (f) Co-immunoprecipitation of epitope tagged mPatched (Patched) or epitope
20 tagged rSmo (Smo) with IgG-SHH-N. (g) cross-linking of 125 I-SHH-N (125 I-SHH) to cells expressing mPatched or rSmo in the absence or presence of unlabeled SHH-N. (h) Co-immunoprecipitation of 125 I-SHH by an epitope tagged mPatched (Patched) or an epitope tagged rSmo (Smo). (i) competition binding of 125 I-SHH to cells expressing mPatched or mPatched plus rSmo.

Figure 7 illustrates (a) Double immunohistochemical staining of Patched (red) and Smo (green) in transfected cells. Yellow indicates co-expression of the two proteins. (b and c) Detection of Patched-Smo Complex by immunoprecipitation. (b) immunoprecipitation with antibodies to the epitope tagged Patched and analysis on a Western blot with antibodies to epitope tagged Smo. (c) immunoprecipitation with antibodies to the epitope tagged Smo and analysis on a Western blot with antibodies to epitope tagged Patched. (d and e) co-immunoprecipitation of 125 I-SHH bound to cells expressing both Smo and Patched with antibodies to
30 either Smo (d) or Patched (e) epitope tags.

Figure 8 shows a Western blot from a SDS-gel depicting the expression level of a wildtype (WT) and mutated Patched (mutant).

Figure 9 shows a model describing the putative SHH receptor and its proposed activation by SHH. As shown in the model, Patched is a ligand binding component and vSmo is a signalling component
35 in a multi-subunit SHH-receptor.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

The terms "vertebrate Smoothened", "vertebrate Smoothened protein" and "vSmo" when used herein encompass native sequence vertebrate Smoothened and vertebrate Smoothened variants (each of

which is defined herein). These terms encompass Smoothened from a variety of animals classified as vertebrates, including mammals. In a preferred embodiment, the vertebrate Smoothened is rat Smoothened (rSmo) or human Smoothened (hSmo). The vertebrate Smoothened may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods.

5 A "native sequence vertebrate Smoothened" comprises a protein having the same amino acid sequence as a vertebrate Smoothened derived from nature. Thus, a native sequence vertebrate Smoothened can have the amino acid sequence of naturally occurring human Smoothened, rat Smoothened, or Smoothened from any other vertebrate. Such native sequence vertebrate Smoothened can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence vertebrate Smoothened" specifically
10 encompasses naturally-occurring truncated forms of the vertebrate Smoothened, naturally-occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of the vertebrate Smoothened. In one embodiment of the invention, the native sequence vertebrate Smoothened is a mature native sequence Smoothened comprising the amino acid sequence of SEQ ID NO:4. In another embodiment of the invention, the native sequence vertebrate Smoothened is a mature native sequence Smoothened comprising the amino acid
15 sequence of SEQ ID NO:2.

"Vertebrate Smoothened variant" means a vertebrate Smoothened as defined below having less than 100% sequence identity with vertebrate Smoothened having the deduced amino acid sequence shown in SEQ ID NO:4 for human Smoothened or SEQ ID NO:2 for rat Smoothened. Such vertebrate Smoothened variants include, for instance, vertebrate Smoothened proteins wherein one or more amino acid residues are
20 added at the N- or C-terminus of, or within, the sequences of SEQ ID NO:4 or SEQ ID NO:2; wherein about one to thirty amino acid residues are deleted, or optionally substituted by one or more amino acid residues; and derivatives thereof, wherein an amino acid residue has been covalently modified so that the resulting product has a non-naturally occurring amino acid. Ordinarily, a vertebrate Smoothened variant will have at least about 80% sequence identity, more preferably at least about 90% sequence identity, and even more preferably at least
25 about 95% sequence identity with the sequence of SEQ ID NO:4 or SEQ ID NO:2.

The term "epitope tag" when used herein refers to a tag polypeptide having enough residues to provide an epitope against which an antibody thereagainst can be made, yet is short enough such that it does not interfere with activity of the vertebrate Smoothened. The tag polypeptide preferably also is fairly unique so that the antibody thereagainst does not substantially cross-react with other epitopes. Suitable tag
30 polypeptides generally have at least six amino acid residues and usually between about 8-50 amino acid residues (preferably between about 9-30 residues).

"Isolated," when used to describe the various proteins disclosed herein, means protein that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic
35 uses for the protein, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous substances. In preferred embodiments, the protein will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated protein includes protein *in situ* within recombinant cells, since at least one component of

the vSmo natural environment will not be present. Ordinarily, however, isolated protein will be prepared by at least one purification step.

An "isolated" vSmo nucleic acid molecule is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the vSmo nucleic acid. An isolated vSmo nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated vSmo nucleic acid molecules therefore are distinguished from the vSmo nucleic acid molecule as it exists in natural cells. However, an isolated vSmo nucleic acid molecule includes vSmo nucleic acid molecules contained in cells that ordinarily express vSmo where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers single anti-vSmo monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies) and anti-vSmo antibody compositions with polyepitopic specificity.

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to conventional (polyclonal) antibody preparations which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen.

The monoclonal antibodies herein include hybrid and recombinant antibodies produced by splicing a variable (including hypervariable) domain of an anti-vSmo antibody with a constant domain (e.g., "humanized" antibodies); or a light chain with a heavy chain, or a chain from one species with a chain from another species, or fusions with heterologous proteins, regardless of species of origin or immunoglobulin class or subclass designation, as well as antibody fragments (e.g., Fab, F(ab')₂, and Fv), so long as they exhibit the desired activity. See, e.g., U.S. Pat. No. 4,816,567 and Mage et al., in Monoclonal Antibody Production Techniques and Applications, pp.79-97 (Marcel Dekker, Inc.: New York, 1987).

Thus, the modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by the hybridoma method first described by Kohler and Milstein, *Nature*, 256:495 (1975), or may be made by recombinant DNA methods such as described in U.S. Pat. No. 4,816,567. The "monoclonal antibodies" may also be isolated from phage libraries generated using the techniques described in McCafferty et al., *Nature*, 348:552-554 (1990), for example.

"Humanized" forms of non-human (*e.g.* murine) antibodies are specific chimeric immunoglobulins, immunoglobulin chains, or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, the humanized antibody may comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. These modifications are made to further refine and optimize antibody performance. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region or domain (Fc), typically that of a human immunoglobulin.

The term "vertebrate" as used herein refers to any animal classified as a vertebrate including certain classes of fish, reptiles, birds, and mammals. The term "mammal" as used herein refers to any animal classified as a mammal, including humans, cows, rats, mice, horses, dogs and cats.

II. Modes For Carrying Out The Invention

The present invention is based on the discovery of vertebrate homologues of Smoothed. In particular, Applicants have identified and isolated human and rat Smoothed. The properties and characteristics of human and rat Smoothed are described in further detail in the Examples below. Based upon the properties and characteristics of human and rat Smoothed disclosed herein, it is Applicants' present belief that vertebrate Smoothed is a signalling component in a multi-subunit Hedgehog (particularly Sonic Hedgehog "SHH") receptor.

A description follows as to how vertebrate Smoothed may be prepared.

35 A. Preparation of vSmo

Techniques suitable for the production of vSmo are well known in the art and include isolating vSmo from an endogenous source of the polypeptide, peptide synthesis (using a peptide synthesizer)

and recombinant techniques (or any combination of these techniques). The description below relates primarily to production of vSmo by culturing cells transformed or transfected with a vector containing vSmo nucleic acid. It is of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare vSmo.

5 1. Isolation of DNA Encoding vSmo

The DNA encoding vSmo may be obtained from any cDNA library prepared from tissue believed to possess the vSmo mRNA and to express it at a detectable level. Accordingly, human Smo DNA can be conveniently obtained from a cDNA library prepared from human tissues, such as the library of human embryonic lung cDNA described in Example 3. Rat Smo DNA can be conveniently obtained from a cDNA
10 library prepared from rat tissues, such as described in Example 1. The vSmo-encoding gene may also be obtained from a genomic library or by oligonucleotide synthesis.

Libraries can be screened with probes (such as antibodies to the vSmo or oligonucleotides or polypeptides as described in the Examples) designed to identify the gene of interest or the protein encoded by it. The probes are preferably labeled such that they can be detected upon hybridization to DNA in the
15 library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ³²P-labeled ATP, biotinylation or enzyme labeling. Screening the cDNA or genomic library with a selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding vSmo is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].
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Nucleic acid having all the protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequences disclosed herein, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

25 vSmo variants can be prepared by introducing appropriate nucleotide changes into the vSmo DNA, or by synthesis of the desired vSmo polypeptide. Those skilled in the art will appreciate that amino acid changes (compared to native sequence vSmo) may alter post-translational processes of the vSmo, such as changing the number or position of glycosylation sites.

Variations in the native sequence vSmo can be made using any of the techniques and
30 guidelines for conservative and non-conservative mutations set forth in U.S. Pat. No. 5,364,934. These include oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis.

2. Insertion of Nucleic Acid into A Replicable Vector

The nucleic acid (*e.g.*, cDNA or genomic DNA) encoding vSmo may be inserted into a replicable vector for further cloning (amplification of the DNA) or for expression. Various vectors are publicly
35 available. The vector components generally include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence, each of which is described below.

(i) Signal Sequence Component

The vSmo may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous amino acid sequence or polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the vSmo DNA that is inserted into the vector. The heterologous signal sequence selected preferably is one that is recognized and processed (*i.e.*, cleaved by a signal peptidase) by the host cell.

(ii) Origin of Replication Component

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Generally, in cloning vectors this sequence is one that enables the vector to replicate independently of the host chromosomal DNA, and includes origins of replication or autonomously replicating sequences. Such sequences are well known for a variety of bacteria, yeast, and viruses.

Most expression vectors are "shuttle" vectors, *i.e.*, they are capable of replication in at least one class of organisms but can be transfected into another organism for expression. For example, a vector is cloned in *E. coli* and then the same vector is transfected into yeast or mammalian cells for expression even though it is not capable of replicating independently of the host cell chromosome.

DNA may also be amplified by insertion into the host genome. This is readily accomplished using *Bacillus* species as hosts, for example, by including in the vector a DNA sequence that is complementary to a sequence found in *Bacillus* genomic DNA. Transfection of *Bacillus* with this vector results in homologous recombination with the genome and insertion of vSmo DNA.

(iii) Selection Gene Component

Expression and cloning vectors typically contain a selection gene, also termed a selectable marker. This gene encodes a protein necessary for the survival or growth of transformed host cells grown in a selective culture medium. Host cells not transformed with the vector containing the selection gene will not survive in the culture medium. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, *e.g.*, ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, *e.g.*, the gene encoding D-alanine racemase for *Bacilli*.

One example of a selection scheme utilizes a drug to arrest growth of a host cell. Those cells that are successfully transformed with a heterologous gene produce a protein conferring drug resistance and thus survive the selection regimen. Examples of such dominant selection use the drugs neomycin [Southern et al., *J. Molec. Appl. Genet.*, 1:327 (1982)], mycophenolic acid [Mulligan et al., *Science*, 209:1422 (1980)] or hygromycin [Sugden et al., *Mol. Cell. Biol.*, 5:410-413 (1985)]. The three examples given above employ bacterial genes under eukaryotic control to convey resistance to the appropriate drug G418 or neomycin (geneticin), xgpt (mycophenolic acid), or hygromycin, respectively.

Another example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the vSmo nucleic acid, such as DHFR or thymidine kinase. The mammalian cell transformants are placed under selection pressure that only the transformants are uniquely

adapted to survive by virtue of having taken up the marker. Selection pressure is imposed by culturing the transformants under conditions in which the concentration of selection agent in the medium is successively changed, thereby leading to amplification of both the selection gene and the DNA that encodes vSmo. Amplification is the process by which genes in greater demand for the production of a protein critical for growth are reiterated in tandem within the chromosomes of successive generations of recombinant cells.

Cells transformed with the DHFR selection gene may first be identified by culturing all of the transformants in a culture medium that contains methotrexate (Mtx), a competitive antagonist of DHFR. An appropriate host cell when wild-type DHFR is employed is the Chinese hamster ovary (CHO) cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). The transformed cells are then exposed to increased levels of methotrexate. This leads to the synthesis of multiple copies of the DHFR gene, and, concomitantly, multiple copies of other DNA comprising the expression vectors, such as the DNA encoding vSmo.

(iv) Promoter Component

Expression and cloning vectors usually contain a promoter that is recognized by the host organism and is operably linked to the vSmo nucleic acid sequence. Promoters are untranslated sequences located upstream (5') to the start codon of a structural gene (generally within about 100 to 1000 bp) that control the transcription and translation of particular nucleic acid sequence, such as the vSmo nucleic acid sequence, to which they are operably linked. Such promoters typically fall into two classes, inducible and constitutive. Inducible promoters are promoters that initiate increased levels of transcription from DNA under their control in response to some change in culture conditions, e.g., the presence or absence of a nutrient or a change in temperature. At this time a large number of promoters recognized by a variety of potential host cells are well known. These promoters are operably linked to vSmo encoding DNA by removing the promoter from the source DNA by restriction enzyme digestion and inserting the isolated promoter sequence into the vector.

Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (trp) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid promoters such as the tac promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)].

Promoter sequences are known for eukaryotes. Virtually all eukaryotic genes have an AT-rich region located approximately 25 to 30 bases upstream from the site where transcription is initiated. Another sequence found 70 to 80 bases upstream from the start of transcription of many genes is a CXCAAT region where X may be any nucleotide. At the 3' end of most eukaryotic genes is an AATAAA sequence that may be the signal for addition of the poly A tail to the 3' end of the coding sequence. All of these sequences are suitably inserted into eukaryotic expression vectors.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase,

phosphoglucose isomerase, and glucokinase. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

vSmo transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and most preferably Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter.

The early and late promoters of the SV40 virus are conveniently obtained as an SV40 restriction fragment that also contains the SV40 viral origin of replication [Fiers et al., *Nature*, 273:113 (1978); Mulligan and Berg, *Science*, 209:1422-1427 (1980); Pavlakis et al., *Proc. Natl. Acad. Sci. USA*, 78:7398-7402 (1981)]. The immediate early promoter of the human cytomegalovirus is conveniently obtained as a HindIII E restriction fragment [Greenaway et al., *Gene*, 18:355-360 (1982)]. A system for expressing DNA in mammalian hosts using the bovine papilloma virus as a vector is disclosed in U.S. Patent No. 4,419,446. A modification of this system is described in U.S. Patent No. 4,601,978 [See also Gray et al., *Nature*, 295:503-508 (1982) on expressing cDNA encoding immune interferon in monkey cells; Reyes et al., *Nature*, 297:598-601 (1982) on expression of human β -interferon cDNA in mouse cells under the control of a thymidine kinase promoter from herpes simplex virus; Canaani and Berg, *Proc. Natl. Acad. Sci. USA* 79:5166-5170 (1982) on expression of the human interferon β 1 gene in cultured mouse and rabbit cells; and Gorman et al., *Proc. Natl. Acad. Sci. USA*, 79:6777-6781 (1982) on expression of bacterial CAT sequences in CV-1 monkey kidney cells, chicken embryo fibroblasts, Chinese hamster ovary cells, HeLa cells, and mouse NIH-3T3 cells using the Rous sarcoma virus long terminal repeat as a promoter].

(v) Enhancer Element Component

Transcription of a DNA encoding the vSmo by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Enhancers are relatively orientation and position independent, having been found 5' [Laimins et al., *Proc. Natl. Acad. Sci. USA*, 78:993 (1981)] and 3' [Lusky et al., *Mol. Cell Bio.*, 3:1108 (1983)] to the transcription unit, within an intron [Banerji et al., *Cell*, 33:729 (1983)], as well as within the coding sequence itself [Osborne et al., *Mol. Cell Bio.*, 4:1293 (1984)]. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. See also Yaniv, *Nature*, 297:17-18 (1982) on enhancing elements for activation of eukaryotic promoters.

(vi) Transcription Termination Component

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also typically contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain

nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding vSmo.

(vii) Construction and Analysis of Vectors

Construction of suitable vectors containing one or more of the above-listed components employs standard ligation techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and re-ligated in the form desired to generate the plasmids required.

For analysis to confirm correct sequences in plasmids constructed, the ligation mixtures can be used to transform *E. coli* K12 strain 294 (ATCC 31,446) and successful transformants selected by ampicillin or tetracycline resistance where appropriate. Plasmids from the transformants are prepared, analyzed by restriction endonuclease digestion, and/or sequenced by the method of Messing et al., Nucleic Acids Res., 9:309 (1981) or by the method of Maxam et al., Methods in Enzymology, 65:499 (1980).

(viii) Transient Expression Vectors

Expression vectors that provide for the transient expression in mammalian cells of DNA encoding vSmo may be employed. In general, transient expression involves the use of an expression vector that is able to replicate efficiently in a host cell, such that the host cell accumulates many copies of the expression vector and, in turn, synthesizes high levels of a desired polypeptide encoded by the expression vector [Sambrook et al., *supra*]. Transient expression systems, comprising a suitable expression vector and a host cell, allow for the convenient positive identification of polypeptides encoded by cloned DNAs, as well as for the rapid screening of such polypeptides for desired properties.

(ix) Suitable Exemplary Vertebrate Cell Vectors

Other methods, vectors, and host cells suitable for adaptation to the synthesis of vSmo in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

3. Selection and Transformation of Host Cells

Suitable host cells for cloning or expressing the DNA in the vectors herein are the prokaryote, yeast, or higher eukaryote cells described above. Suitable prokaryotes for this purpose include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *Escherichia*. Preferably, the host cell should secrete minimal amounts of proteolytic enzymes.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast may be suitable cloning or expression hosts for vSmo-encoding vectors. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms. However, a number of other genera, species, and strains are commonly available and useful herein.

Suitable host cells for the expression of glycosylated vSmo are derived from multicellular organisms. Such host cells are capable of complex processing and glycosylation activities. In principle, any higher eukaryotic cell culture is workable, whether from vertebrate or invertebrate culture. Examples of invertebrate cells include plant and insect cells.

Propagation of vertebrate cells in culture (tissue culture) is also well known in the art [See, e.g., Tissue Culture, Academic Press, Kruse and Patterson, editors (1973)]. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human

embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture. Graham et al., J. Gen Virol., 36:59 (1977)); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO. Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4. Mather, Biol. Reprod., 23:243-251 (1980)); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); mouse mammary tumor (MMT 060562, ATCC CCL51); TRI cells (Mather et al., Annals N.Y. Acad. Sci., 383:44-68 (1982)); MRC 5 cells; and FS4 cells.

Host cells are transfected and preferably transformed with the above-described expression or cloning vectors for vSmo production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

Transfection refers to the taking up of an expression vector by a host cell whether or not any coding sequences are in fact expressed. Numerous methods of transfection are known to the ordinarily skilled artisan, for example, CaPO_4 and electroporation. Successful transfection is generally recognized when any indication of the operation of this vector occurs within the host cell.

Transformation means introducing DNA into an organism so that the DNA is replicable, either as an extrachromosomal element or by chromosomal integrant. Depending on the host cell used, transformation is done using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes or other cells that contain substantial cell-wall barriers. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. In addition, plants may be transfected using ultrasound treatment as described in WO 91/00358 published 10 January 1991.

For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) is preferred. General aspects of mammalian cell host system transformations have been described in U.S. Pat. No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

4. Culturing the Host Cells

Prokaryotic cells used to produce vSmo may be cultured in suitable media as described generally in Sambrook et al., supra.

The mammalian host cells used to produce vSmo may be cultured in a variety of media. Examples of commercially available media include Ham's F10 (Sigma), Minimal Essential Medium ("MEM", Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium ("DMEM", Sigma). Any such media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such

as HEPES), nucleosides (such as adenosine and thymidine), antibiotics (such as GentamycinTM drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art. The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

In general, principles, protocols, and practical techniques for maximizing the productivity of mammalian cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991).

The host cells referred to in this disclosure encompass cells in culture as well as cells that are within a host animal.

5. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Various labels may be employed, most commonly radioisotopes, and particularly ³²P. However, other techniques may also be employed, such as using biotin-modified nucleotides for introduction into a polynucleotide. The biotin then serves as the site for binding to avidin or antibodies, which may be labeled with a wide variety of labels, such as radionucleotides, fluorescers or enzymes. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. With immunohistochemical staining techniques, a cell sample is prepared, typically by dehydration and fixation, followed by reaction with labeled antibodies specific for the gene product coupled, where the labels are usually visually detectable, such as enzymatic labels, fluorescent labels, or luminescent labels.

Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence vSmo protein or against a synthetic peptide based on the DNA sequences provided herein.

6. Purification of vSmo

It is contemplated that it may be desired to purify some form of vSmo from recombinant cell proteins or polypeptides to obtain preparations that are substantially homogeneous as to vSmo. As a first step, the culture medium or lysate may be centrifuged to remove particulate cell debris. vSmo thereafter may be purified from contaminant soluble proteins and polypeptides, with the following procedures being exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse

phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; and protein A Sepharose columns to remove contaminants such as IgG. vSmo variants may be recovered in the same fashion as native sequence vSmo, taking account of any substantial changes in properties occasioned by the variation.

- 5 A protease inhibitor such as phenyl methyl sulfonyl fluoride (PMSF) also may be useful to inhibit proteolytic degradation during purification, and antibiotics may be included to prevent the growth of adventitious contaminants.

7. Covalent Modifications of vSmo

- Covalent modifications of vSmo are included within the scope of this invention. One type
10 of covalent modification of the vSmo included within the scope of this invention comprises altering the native glycosylation pattern of the protein. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence vSmo, and/or adding one or more glycosylation sites that are not present in the native sequence vSmo.

- Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to
15 the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tripeptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tripeptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose to a
20 hydroxylamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

- Addition of glycosylation sites to the vSmo may be accomplished by altering the amino acid sequence such that it contains one or more of the above-described tripeptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine
25 or threonine residues to the native sequence vSmo (for O-linked glycosylation sites). The vSmo amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the vSmo protein at preselected bases such that codons are generated that will translate into the desired amino acids. The DNA mutation(s) may be made using methods described above and in U.S. Pat. No. 5,364,934, supra.

- Another means of increasing the number of carbohydrate moieties on the vSmo is by
30 chemical or enzymatic coupling of glycosides to the polypeptide. Depending on the coupling mode used, the sugar(s) may be attached to (a) arginine and histidine, (b) free carboxyl groups, (c) free sulfhydryl groups such as those of cysteine, (d) free hydroxyl groups such as those of serine, threonine, or hydroxyproline, (e) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan, or (f) the amide group of glutamine. These methods are described in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).
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Removal of carbohydrate moieties present on the vSmo protein may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. For instance, chemical deglycosylation by exposing the polypeptide to the

compound trifluoromethanesulfonic acid, or an equivalent compound can result in the cleavage of most or all sugars except the linking sugar (N-acetylglucosamine or N-acetylgalactosamine), while leaving the polypeptide intact. Chemical deglycosylation is described by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Glycosylation at potential glycosylation sites may be prevented by the use of the compound tunicamycin as described by Duskin et al., J. Biol. Chem., 257:3105 (1982). Tunicamycin blocks the formation of protein-N-glycoside linkages.

8. vSmo Chimeras

The present invention also provides chimeric molecules comprising vSmo fused to another, heterologous amino acid sequence or polypeptide. In one embodiment, the chimeric molecule comprises a fusion of the vSmo with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally provided at the amino- or carboxyl- terminus of the vSmo. Such epitope-tagged forms of the vSmo are desirable as the presence thereof can be detected using a labeled antibody against the tag polypeptide. Also, provision of the epitope tag enables the vSmo to be readily purified by affinity purification using the anti-tag antibody. Affinity purification techniques and diagnostic assays involving antibodies are described later herein.

Tag polypeptides and their respective antibodies are well known in the art. Examples include the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides have been disclosed. Examples include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an α -tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)]. Once the tag polypeptide has been selected, an antibody thereto can be generated using the techniques disclosed herein.

The general methods suitable for the construction and production of epitope-tagged vSmo are the same as those disclosed hereinabove. vSmo-tag polypeptide fusions are most conveniently constructed by fusing the cDNA sequence encoding the vSmo portion in-frame to the tag polypeptide DNA sequence and expressing the resultant DNA fusion construct in appropriate host cells. Ordinarily, when preparing the vSmo-tag polypeptide chimeras of the present invention, nucleic acid encoding the vSmo will be fused at its 3' end to nucleic acid encoding the N-terminus of the tag polypeptide, however 5' fusions are also possible.

9. Methods of Using vSmo

vSmo, as disclosed in the present specification, has utility in therapeutic and non-therapeutic applications. As a therapeutic, vSmo (or the nucleic acid encoding the same) can be employed in *in vivo* or *ex vivo* gene therapy techniques. In non-therapeutic applications, nucleic acid sequences encoding the vSmo may be used as a diagnostic for tissue-specific typing. For example, procedures like *in situ* hybridization,

Northern and Southern blotting, and PCR analysis may be used to determine whether DNA and/or RNA encoding vSmo is present in the cell type(s) being evaluated. vSmo nucleic acid will also be useful for the preparation of vSmo by the recombinant techniques described herein.

The isolated vSmo may be used in quantitative diagnostic assays as a control against which samples containing unknown quantities of vSmo may be prepared. vSmo preparations are also useful in generating antibodies, as standards in assays for vSmo (e.g., by labeling vSmo for use as a standard in a radioimmunoassay, radioreceptor assay, or enzyme-linked immunoassay), and in affinity purification techniques.

Nucleic acids which encode vSmo, such as the rat vSmo disclosed herein, can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, rat cDNA encoding rSmo or an appropriate sequence thereof can be used to clone genomic DNA encoding Smo in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding Smo. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for vSmo transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding vSmo introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding vSmo. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with constitutive activity of vSmo or Hedgehog, including some forms of cancer that may result therefrom, such as for example, basal cell carcinoma, basal cell nevus syndrome and pancreatic carcinoma. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, the non-human homologues of vSmo can be used to construct a vSmo "knock out" animal which has a defective or altered gene encoding vSmo as a result of homologous recombination between the endogenous gene encoding vSmo and altered genomic DNA encoding vSmo introduced into an embryonic cell of the animal. For example, rat cDNA encoding Smo can be used to clone genomic DNA encoding Smo in accordance with established techniques. A portion of the genomic DNA encoding Smo can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem*

Cells: A Practical Approach, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and can be used in the study of the mechanism by which the Hedgehog family of molecules exerts mitogenic, differentiative, and morphogenic effects.

B. Anti-vSmo Antibody Preparation

The present invention further provides anti-vSmo antibodies. Antibodies against vSmo may be prepared as follows. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

The vSmo antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the vSmo protein or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins which may be employed include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. An aggregating agent such as alum may also be employed to enhance the mammal's immune response. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation. The mammal can then be bled, and the serum assayed for antibody titer. If desired, the mammal can be boosted until the antibody titer increases or plateaus.

2. Monoclonal Antibodies

The vSmo antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *supra*. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized (such as described above) with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the vSmo protein or a fusion protein thereof. Cells expressing vSmo at their surface may also be employed. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse

myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Rockville, Maryland. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, *J. Immunol.*, **133**:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against vSmo. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, **107**:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, *supra*]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an

antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art. For instance, digestion can be performed using papain. Examples of papain digestion are described in WO 94/29348 published 12/22/94 and U.S. Patent No. 4,342,566. Papain digestion of antibodies typically produces two identical antigen binding fragments, called Fab fragments, each with a single antigen binding site, and a residual Fc fragment. Pepsin treatment yields an F(ab')₂ fragment that has two antigen combining sites and is still capable of cross-linking antigen.

The Fab fragments produced in the antibody digestion also contain the constant domains of the light chain and the first constant domain (CH₁) of the heavy chain. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH₁ domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

3. Humanized Antibodies

The vSmO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Reichmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

The choice of human variable domains, both light and heavy, to be used in making the humanized antibodies is very important in order to reduce antigenicity. According to the "best-fit" method, the sequence of the variable domain of a rodent antibody is screened against the entire library of known human variable domain sequences. The human sequence which is closest to that of the rodent is then accepted as the human framework (FR) for the humanized antibody [Sims et al., J. Immunol., 151:2296 (1993); Chothia and Lesk, J. Mol. Biol., 196:901 (1987)]. Another method uses a particular framework derived from the consensus sequence of all human antibodies of a particular subgroup of light or heavy chains. The same framework may be used for several different humanized antibodies [Carter et al., Proc. Natl. Acad. Sci. USA, 89:4285 (1992); Presta et al., J. Immunol., 151:2623 (1993)].

It is further important that antibodies be humanized with retention of high affinity for the antigen and other favorable biological properties. To achieve this goal, according to a preferred method, humanized antibodies are prepared by a process of analysis of the parental sequences and various conceptual humanized products using three dimensional models of the parental and humanized sequences. Three dimensional immunoglobulin models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate immunoglobulin sequences. Inspection of these displays permits analysis of the likely role of the residues in the functioning of the candidate immunoglobulin sequence, i.e., the analysis of residues that influence the ability of the candidate immunoglobulin to bind its antigen. In this way, FR residues can be selected and combined from the consensus and import sequence so that the desired antibody characteristic, such as increased affinity for the target antigen(s), is achieved. In general, the CDR residues are directly and most substantially involved in influencing antigen binding [see, WO 94/04679 published 3 March 1994].

Transgenic animals (e.g., mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production can be employed. For example, it has been described that the homozygous deletion of the antibody heavy chain joining region (J_H) gene in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array in such germ-line mutant mice will result in the production of human antibodies upon antigen challenge [see, e.g., Jakobovits et al., Proc. Natl.

Acad. Sci. USA, 90:2551-255 (1993); Jakobovits et al., Nature, 362:255-258 (1993); Bruggermann et al., Year in Immuno., 7:33 (1993)]. Human antibodies can also be produced in phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)]. The techniques of Cote et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cote et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)].

4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the vSmo, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Millstein and Cuello, Nature, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., EMBO J., 10:3655-3659 (1991).

According to a different and more preferred approach, antibody variable domains with the desired binding specificities (antibody-antigen combining sites) are fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. This provides for great flexibility in adjusting the mutual proportions of the three polypeptide fragments in embodiments when unequal ratios of the three polypeptide chains used in the construction provide the optimum yields. It is, however, possible to insert the coding sequences for two or all three polypeptide chains in one expression vector when the expression of at least two polypeptide chains in equal ratios results in high yields or when the ratios are of no particular significance. In a preferred embodiment of this approach, the bispecific antibodies are composed of a hybrid immunoglobulin heavy chain with a first binding specificity in one arm, and a hybrid immunoglobulin heavy-chain/light-chain pair (providing a second binding specificity) in the other arm. It was found that this asymmetric structure facilitates the separation of the desired bispecific compound from unwanted immunoglobulin chain combinations, as the presence of an immunoglobulin light chain in only one half of the bispecific molecule provides for a facile way of separation. This approach is disclosed in WO 94/04690 published 3 March 1994. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [US Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Pat. No. 4,676,980.

6. Uses of vSmo Antibodies

vSmo antibodies may be used in diagnostic assays for vSmo, *e.g.*, detecting its expression in specific cells or tissues. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, Monoclonal Antibodies: A Manual of Techniques, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

vSmo antibodies also are useful for the affinity detection or purification of vSmo from recombinant cell culture or natural sources. In this process, the antibodies against vSmo are immobilized on a suitable support, such as a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the vSmo, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the vSmo, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the vSmo from the antibody.

The vSmo antibodies may also be employed as therapeutics. For example, vSmo antibodies may be used to block or neutralize excess vSmo signalling that may result from mutant or inactivated Patched. Accordingly, the vSmo antibodies may be used in the treatment of, or amelioration of symptoms caused by, a pathological condition resulting from or associated with excess vSmo or vSmo signalling. Optionally, agonistic vSmo antibodies can be employed to induce the formation of, or enhance or stimulate tissue regeneration, such as regeneration of skin tissue, lung tissue, muscle (such as heart or skeletal muscle), neural tissue (such as serotonergic neurons, motoneurons or striatal neurons), bone tissue or gut tissue. This vSmo antibody therapy will be useful in instances where the tissue has been damaged by disease, aging or trauma.

The vSmo antibodies may be used or administered to a patient in a pharmaceutically-acceptable carrier. Suitable carriers and their formulations are described in Remington's Pharmaceutical Sciences, 16th ed., 1980, Mack Publishing Co., edited by Oslo et al. If the vSmo antibodies are to be administered to a patient, the antibodies can be administered by injection (e.g., intravenous, intraperitoneal, subcutaneous, intramuscular), or by other methods such as infusion that ensure its delivery to the bloodstream in an effective form. Effective dosages and schedules for administering the vSmo antibodies may be determined empirically, and making such determinations is within the skill in the art. Those skilled in the art will understand that the dosage of vSmo antibodies that must be administered will vary depending on, for example, the patient which will receive the antibodies, the route of administration, and other therapeutic agents being administered to the mammal. Guidance in selecting appropriate doses for such vSmo-antibodies is found in the literature on therapeutic uses of antibodies, e.g., Handbook of Monoclonal Antibodies, Ferrone et al., eds., Noyes Publications, Park Ridge, N.J., (1985) ch. 22 and pp. 303-357; Smith et al., Antibodies in Human Diagnosis and Therapy, Haber et al., eds., Raven Press, New York (1977) pp. 365-389. A typical daily dosage of the vSmo antibodies used alone might range from about 1 μ g/kg to up to 100 mg/kg of body weight or more per day, depending on the factors mentioned above.

C. Kits Containing vSmo or vSmo Antibodies

In another embodiment of the invention, there are provided articles of manufacture and kits containing vSmo or vSmo antibodies. The article of manufacture typically comprises a container with a label. Suitable containers include, for example, bottles, vials, and test tubes. The containers may be formed from a variety of materials such as glass or plastic. The container holds the vSmo or vSmo antibodies. The label on the container may indicate directions for either *in vivo* or *in vitro* use, such as those described above.

The kit of the invention will typically comprise the container described above and one or more other containers comprising materials desirable from a commercial and user standpoint, including buffers, diluents, filters, and package inserts with instructions for use.

D. Additional Compositions of Matter

In a further embodiment of the invention, there are provided protein complexes comprising vertebrate Smoothened protein and vertebrate Patched protein. As demonstrated in the Examples, vertebrate Smoothened and vertebrate Patched can form a complex. The protein complex which includes vertebrate Smoothened and vertebrate Patched may also include vertebrate Hedgehog protein. Typically in such a complex, the vertebrate Hedgehog binds to the vertebrate Patched but does not bind to the vertebrate Smoothened. In a preferred embodiment, the complex comprising vertebrate Smoothened and vertebrate Patched is a receptor for vertebrate Hedgehog.

The invention also provides a vertebrate Patched which binds to vertebrate Smoothened. Optionally the vertebrate Patched comprises a sequence which is a derivative of or fragment of a native sequence vertebrate Patched. The vertebrate Patched will typically consist of a sequence which has less than 100% sequence identity with a native sequence vertebrate Patched. In one embodiment, the vertebrate Patched directly and specifically binds vertebrate Smoothened. Alternatively, it is contemplated that the vertebrate Patched may bind vertebrate Smoothened indirectly.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

All commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Rockville, Maryland.

EXAMPLE 1

Isolation and Cloning of Rat Smoothened cDNA

Full-length rat Smoothened cDNA was isolated by low stringency hybridization screening of 1.2×10^6 plaques of an embryonic day 9-10 rat cDNA library (containing cDNAs size-selected >1500 base pairs), using the entire coding region of Drosophila Smoothened [Alcedo et. al., *supra*] (labeled with ^{32}P -dCTP) as a probe. The library was prepared by cloning cDNA inserts into the NotI site of a lambda RK18 vector [Klein et. al., *Proc. Natl. Acad. Sci.*, 93:7108-7113 (1996)] following XmnI adapters ligation. Conditions for hybridization were: 5 x SSC, 30% formamide, 5 x Denhardt's, 50 mM sodium phosphate (pH 6.5), 5% dextran sulfate, 0.1% SDS and 50 $\mu\text{g/ml}$ salmon sperm DNA, overnight at 42°C . Nitrocellulose filters were washed to a stringency of 1 x SSC at 42°C , and exposed overnight to Kodak X-AR film. Three of eight positive plaques were selected for further purification. After amplification of the plaque-purified phage, phagemid excision products were generated by growing M13 helper phage (M13K07; obtained from New England Biolabs), bacteria (BB4; obtained from Stratagene), and the purified phage together in a 100:10:1 ratio. Plasmid DNA was recovered by Qiagen purification from ampicillin-resistant colonies following infection of BB4 with the excised purified phagemid.

Sequencing of the three cDNAs showed them to be identical, with the exception that two contained only a partial coding sequence, whereas the third contained the entire open reading frame of rat Smoothened, including 449 and 1022 nucleotides, respectively of 5' and 3' untranslated sequence and a poly-A tail. This cDNA clone was sequenced completely on both strands.

The entire nucleotide sequence of rat Smoothened (rSmo) is shown in Figure 1 (SEQ ID NO:1) (reference is also made to Applicants' ATCC deposit of the rat Smoothened in pRK5.rsmo.AR140, assigned ATCC Dep. No. 98165). The cDNA contained an open reading frame with a translational initiation site assigned to the ATG codon at nucleotide positions 450-452. The open reading frame ends at the termination codon at nucleotide positions 2829-2831.

The predicted amino acid sequence of the rat Smoothened (rSmo) contains 793 amino acids (including a 32 amino acid signal peptide), as shown in Figure 1 (SEQ ID NO:2). rSmo appears to be a typical seven transmembrane (7 TM), G protein-coupled receptor, containing 4 potential N-glycosylation sites and a 203 amino acid long putative extracellular amino-terminus domain which contains 13 stereotypically spaced cysteines (see Fig. 2).

An alignment of the rSmo sequence with sequences for dSmo, wingless receptor and vertebrate Frizzled revealed that rSmo is 33% homologous to the dSmo sequence reported in Alcedo et al., supra (50% homologous in the transmembrane domains); 23% homologous to the wingless receptor sequence reported in Bhanot et al., supra; and 25% homologous to the vertebrate Frizzled sequence reported in Chan et al., supra.

EXAMPLE 2

In Situ Hybridization and Northern Blot Analysis

In situ hybridization and Northern blot analyses were conducted to examine tissue distribution of Smo, Patched and SHH in embryonic and adult rat tissues.

For *in situ* hybridization, E9-E15.5 rat embryos (Hollister Labs) were immersion-fixed overnight at 4°C in 4% paraformaldehyde, then cryoprotected overnight in 20% sucrose. Adult rat brains and spinal cords were frozen fresh. All tissues were sectioned at 16 µm, and processed for *in situ* hybridization using ³³P-UTP labelled RNA probes as described in Treanor et al., Nature, 382:80-83 (1996). Sense and antisense probes were derived from the N-terminal region of rSmo using T7 polymerase. The probe used to detect SHH was antisense to bases 604-1314 of mouse SHH [Echelard et al., Cell, 75:1417-1430 (1993)]. The probe used to detect Patched was antisense to bases 502-1236 of mouse Patched [Goodrich et al., supra]. Reverse transcriptase polymerase chain reaction analysis was performed as described in Treanor et al., supra.

For Northern blot analysis, a rat multiple tissue Northern blot (Clontech) was hybridized and washed at high stringency according to the manufacturer's protocol, using a ³²P-dCTP-labelled probe encompassing the entire rSmo coding region.

The results are illustrated in Figure 3. By *in situ* hybridization and Northern blot analysis, expression of rSmo mRNA was detected from E9 onward in SHH responsive tissues such as the neural folds and early neural tube [Echelard et al., supra; Krauss et al., supra]; Roelink et al., supra], pre-somitic mesoderm and somites [Johnson et al., supra; Fan et al., supra], and developing limb buds [Riddle et al., supra]; gut [Roberts et al., supra] and eye [Krauss et al., supra]. Rat Smo transcripts were also found in tissues whose development is regulated by other members of the vertebrate HH protein family such as testes (desert HH) [Bitgood et al., Curr. Biol., 6:298-304 (1996)], cartilage (indian HH) [Vortkamp et al., Science, 273:613-622 (1996)], and muscle (the zebra fish, *echinida* HH) [Currie and Ingham, Nature, 382:452-455 (1996)] (See e.g., Fig. 3; other data not shown). In all of the above recited tissues, rSmo appeared to be co-expressed with rPatched.

rSmo and rPatched mRNAs were also found in and around SHH expressing cells in the embryonic lung, epiglottis, thymus, vertebral column, tongue, jaw, taste buds and teeth (Fig. 3). In the embryonic nervous system, rSmo and rPatched are initially expressed throughout the neural plate; by E12, however, their expression declines in lateral parts of the neural tube, and by P1, was restricted to cells in relatively close proximity to the ventricular zone (Fig. 3). In the adult rat tissues, rSmo expression was maintained in the brain, lung, kidney, testis, heart and spleen (data not shown).

EXAMPLE 3Isolation and Cloning of Human Smoothened cDNA

A cDNA probe corresponding to the coding region of the rat *smoothened* gene (described in Example 1 above) was labeled by the random hexanucleotide method and used to screen 10^6 clones of a human embryonic lung cDNA library (Clontech, Inc.) in λ gt10. Duplicate filters were hybridized at 42°C in 50% formamide, 5x SSC, 10x Denhardt's, 0.05M sodium phosphate (pH 6.5), 0.1% sodium pyrophosphate, 50 mg/ml of sonicated salmon sperm DNA. Filters were rinsed in 2x SSC and then washed once in 0.5x SSC, 0.1% SDS at 42°C. Hybridizing phage were plaque-purified and the cDNA inserts were subcloned into pUC 118 (New England Biolabs). Two clones, 5 and 14, had overlapping inserts of approximately 2 and 2.8 kb respectively, covering the entire human Smoothened coding sequence (See Fig. 4). Clones 5 and 14 have been deposited by Applicants with ATCC as puc.118.hsmo.5 and puc.118.hsmo.14, respectively, and assigned ATCC Dep. Nos. 98162 and 98163, respectively. Both strands were sequenced by standard fluorescent methods on an ABI377 automated sequencer.

The entire nucleotide sequence of human Smoothened is shown in Figure 4 (SEQ ID NO:3). The cDNA contained an open reading frame with a translational initiation site assigned to the ATG codon at nucleotide positions 13-15. The open reading frame ends at the termination codon at nucleotide positions 2374-2376.

The predicted amino acid sequence of the human Smoothened (hSmo) contains 787 amino acids (including a 29 amino acid signal peptide), as shown in Figure 4 (SEQ ID NO:4). hSmo appears to be a typical seven transmembrane (7 TM), G protein-coupled receptor, containing 5 potential N-glycosylation sites and a 202 amino acid long putative extracellular amino-terminus domain which contains 13 stereotypically spaced cysteines.

An alignment of the predicted hSmo amino acid sequence and rSmo sequence (see Example 1) revealed 94% amino acid identity. An alignment of the hSmo sequence with sequences for dSmo, wingless receptor and vertebrate Frizzled revealed that hSmo is 33% homologous to the dSmo sequence reported in Alcedo et al., *supra* (50% homologous in the transmembrane domains); 23% homologous to the wingless receptor sequence reported in Bhanot et al., *supra*; and 25% homologous to the vertebrate Frizzled sequence reported in Chan et al., *supra*. See Figure 5 for a comparison of the primary sequences of human Smo, rat Smo and Drosophila Smo.

30 EXAMPLE 4

Competitive binding, Co-immunoprecipitation,
and Cross-linking Assays

Competitive binding, co-immunoprecipitation and cross-linking assays were conducted to characterize physical association or binding between SHH and rSmo, and between certain biologically active forms of SHH and cells expressing rSmo, mPatched, or both rSmo and mPatched.

1. Materials and Methods

Complementary DNAs for rSmo (described in Example 1); dSmo (described in Alcedo et al., *supra*); Desert HH (described in Echelard et al., *supra*); and murine Patched (described in Goodrich et al., *supra*) were cloned into pRK5 vectors, and epitope tags [Flag epitope tag (Kodak/IBI) and Myc epitope tag (9E10 epitope: InVitrogen)] added to the extreme C-terminus by PCR-based mutagenesis.

SHH-N is the biologically active amino terminus portion of SHH [Lee et al., *Science*, 266:1528-1537 (1994)]. SHH-N was produced as described by Hynes et al., *supra*. A radiolabeled form of SHH-N, ^{125}I SHH-N, was employed.

For IgG-SHH-N production, human embryonic kidney 293 cells were transiently transfected with the expression vector encoding SHH-N fused in frame after amino acid residue 198 to the Fc portion of human IgG-gamma1.

Cells were maintained in serum-free media (OptiMEM: Gibco BRL) for 48 hours. The media was then collected and concentrated 10-fold using a centricon-10 membrane. Conditioned media was used at a concentration of 2x.

Binding assays were conducted to test binding between cells expressing rSmo or dSmo and (1) epitope tagged SHH-N, (2) an IgG-SHH-N chimera, and (3) an epitope tagged Desert HH.

For visualization of SHH binding, COS-7 cells (Genentech, Inc.) transiently expressing rSmo or mPatched (murine Patched) were exposed to epitope tagged SHH-N (2 hours at 4°C), washed 4 times with PBS, then fixed and stained with a cy3-conjugated anti-human IgG (Jackson ImmunoResearch) (for IgG-SHH-N) or anti-Flag M2 antibody (Kodak/IBI) (for Flag-tagged SHH-N).

For immunohistochemistry, COS-7 cells transiently transfected with expression constructs were fixed (10 minutes in 2% paraformaldehyde/0.2% Triton-X 100) and stained using monoclonal anti-Flag M2 antibody (IBI) or anti-Myc antibody (InVitrogen), followed by cy3-conjugated anti-mouse IgG (Jackson ImmunoResearch).

For cross-linking, cells were resuspended at a density of $1-2 \times 10^6/\text{ml}$ in ice-cold L15 media containing 0.1% BSA and 50 pM ^{125}I -labeled SHH (with or without a 1000-fold excess of unlabeled SHH) and incubated at 4°C for 2 hr. 10 mM 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide HCl and 5 mM N-hydroxysulfosuccinimide (Pierce Chemical) were added to the samples and incubated at room temperature for 30 minutes. The cells were then washed 3 times with 1 ml of PBS. Cells were then lysed in lysis buffer [1% Brij-96 (Sigma), 50 mM Tris, pH 8.0, 150 mM NaCl, 1 mM PMSF, 10 μM aprotinin, 10 μM leupeptin] and the protein complexes were immunoprecipitated with antibodies to the epitope tags as indicated. Immunoprecipitated proteins were resuspended in sample buffer (80 mM Tris-HCl [pH 6.8], 10% [v/v] glycerol, 1% [w/v] SDS, 0.025% Bromphenol Blue, denatured and run on 4% SDS-polyacrylamide gels, which were dried and exposed to film.

For the equilibrium binding analysis, the cells were processed as above, and incubated with 50 pM ^{125}I -SHH and various concentrations of cold SHH-N (Cold Ligand). The IGOR program was used to determine K_d .

2. Results

The results are shown in Figure 6. No binding of epitope tagged SHH-N, of IgG-SHH-N chimeric protein or of an epitope tagged Desert HH to cells expressing rSmo or dSmo was observed (Figures 6a-b and data not shown). This data (and the data described below) indicated that rSmo, acting alone, would not likely be a receptor for SHH or Desert HH. However, it was hypothesized that rSmo is a component in a multi-subunit SHH receptor complex and that the ligand binding function of this receptor complex would be provided by another membrane protein such as Patched.

Binding assays were also conducted to test binding between cells expressing rSmo or murine patched and (1) an epitope tagged SHH and (2) an IgG-SHH-N chimera. The data shows that epitope tagged SHH-N as well as an IgG-SHH-N chimeric protein bind specifically and reversibly to cells expressing the mouse Patched (mPatched) (mPatched is 33% identical to Drosophila Patched) (Figure. 6c-e). Furthermore, only mPatched could be immunoprecipitated by the IgG-SHH-N protein (Fig. 6f) and antibodies to an epitope tagged mPatched readily co-immunoprecipitated ^{125}I -SHH-N (Fig. 6h) (antibodies to epitope tagged rSmo could not immunoprecipitate ^{125}I -SHH-N and the IgG-SHH-N chimera did not immunoprecipitate rSmo).

As shown in Fig. 6g, the cross-linking assay of ^{125}I -SHH-N to cells expressing rSmo or mPatched in the presence or absence of cold SHH-N revealed that ^{125}I -SHH-N is cross-linked only to mPatched expressing cells.

The competitive binding assay of ^{125}I -SHH-N and cells expressing mPatched or mPatched plus rSmo also showed that mPatched and SHH-N had a relatively high affinity of interaction (approximate K_d of 460 pM) (Fig. 6i). This corresponds well to the concentrations of SHH-N which are required to elicit biological responses in multiple systems [Fan et al., *supra*; Hynes et al. *supra*; Roelink et al., *supra*]. No binding to cells expressing rSmo alone was observed (data not shown) and there was no increase in binding affinity to mPatched in the presence of rSmo.

EXAMPLE 5

Co-immunoprecipitation Assays

To determine whether Patched and Smo form or interact in a physical complex, co-immunoprecipitation experiments were performed.

1. Materials and Methods

For the double immunohistochemistry, COS-7 cells transiently transfected with expression constructs were permeabilized using 0.2% Triton-x 100. The cells were fixed (10 minutes in 2% paraformaldehyde/0.2% Triton-X 100) and stained using monoclonal anti-Flag M2 antibody (IBI) and rabbit polyclonal anti-Myc primary antibodies (Santa Cruz Biotech), followed by cy3-conjugated anti-mouse IgG (Jackson ImmunoResearch) and bodipy-conjugated anti-rabbit IgG secondary antibodies (Molecular Probes, Inc.).

Human embryonic kidney 293 cells were transiently transfected with expression vectors for epitope tagged rSmo (Flag epitope) and mPatched (Myc epitope) and the resulting proteins complexes were immunoprecipitated with antibody to one of the epitopes and then analyzed on a western blot.

For the co-immunoprecipitation assay, lysates from 293 embryonic kidney cells transiently expressing Flag-tagged rSmo, Myc-tagged mPatched or a combination of the two proteins were incubated (48 hours after transfection) in the presence or absence of the IgG-SHH-N chimera (1 $\mu\text{g}/\text{ml}$, 30 minutes at 37°C) or in the presence of ^{125}I -SHH-N with or without an excess of cold SHH-N (2 hours at 4°C). The incubated samples were then washed 3 times with PBS, and lysed in lysis buffer (see Example 4) as described by Davis et al., *Science*, 259:1736-1739 (1993). The cell lysates were centrifuged at 10,000 rpm for 10 minutes, and the soluble protein complexes were immunoprecipitated with either protein A sepharose (for the IgG-SHH-N), or anti-Flag or anti-Myc antibodies followed by protein A sepharose (for the epitope-tagged rSmo or mPatched, respectively).

The samples were heated to 100°C for 5 minutes in denaturing SDS sample buffer (125 mM Tris, pH 6.8, 2% SDS, 10% glycerol, 100 mM β-mercaptoethanol, 0.05% bromophenol blue) and subjected to SDS-PAGE. The proteins were detected either by exposure of the dried gel to film (for ¹²⁵I-SHH-N) or by blotting to nitrocellulose and probing with antibodies to Flag or Myc epitopes using the ECL detection system (Amersham).

2. Results

The results are illustrated in Figure 7. In cells expressing mPatched alone, or rSmo alone, no co-immunoprecipitated protein complexes could be detected. In contrast, in cells that expressed both mPatched and rSmo (Fig. 7a), rSmo was readily co-immunoprecipitated by antibodies to the epitope tagged mPatched (Fig. 7b) and mPatched was co-immunoprecipitated by antibodies to the epitope tagged rSmo (Fig. 7c).

The ¹²⁵I-SHH-N was readily co-immunoprecipitated by antibodies to the epitope tagged rSmo or mPatched from cells that expressed both rSmo and mPatched, but not from cells expressing rSmo alone (Figs. 7d and 7e). These results indicate that SHH-N, rSmo and mPatched are present in the same physical complex, and that a rSmo-SHH complex does not form in the absence of mPatched. Although not fully understood and not being bound by any particular theory, it is believed that Patched is a ligand binding component and vSmo is a signalling component in a multi-subunit SHH receptor (See, Fig. 9). Patched is also believed to be a negative regulator of vSmo.

EXAMPLE 6

Hahn et al., *supra*, Johnson et al., *supra*, and Gailani et al., *supra*, report that Patched mutations have been associated with BCNS and sporadic basal cell carcinoma ("BCC"). These investigators also report that most of the Patched mutations in BCNS are truncations in which no functional protein is produced. It is believed that BCNS and BCC may be caused or associated with constitutive activation of vSmo, following its release from negative regulation by Patched.

Expression levels of wild-type (native) murine Patched and a mutant Patched were examined. A Patched mutant was generated by site-directed mutagenesis of the wild-type mouse Patched cDNA (described in Example 4) and verified by sequencing. The mutant Patched contained a 3 amino acid insertion (Pro-Asn-Ile) after amino acid residue 815 (this mutant was found in a BCNS family, see, Hahn et al., *supra*). For analysis of protein expression, equal amounts of pRK5 expression vectors containing wild-type or mutant Patched were transfected into 293 cells, and an equal number of cells (2×10^6) were lysed per sample. Proteins were immunoprecipitated from cell lysates by antibody to the Patched epitope tag (myc) and detected on a Western blot with the same antibody.

Applicants found that expression of the mutant Patched (which retains a complete open reading frame) was reduced at least 10-fold as compared to its wild-type counterpart. See Fig. 8.

* * * * *

Deposit of Material

The following materials have been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, USA (ATCC):

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
5	puc.118.hsmo.5	98162	Sept. 6, 1996
	puc.118.hsmo.14	98163	Sept. 6, 1996
	pRK5.rsmo.AR140	98165	Sept. 10, 1996

This deposit was made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposit will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC §122 and the Commissioner's rules pursuant thereto (including 37 CFR §1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Genentech, Inc.
- (ii) TITLE OF INVENTION: Vertebrate Smoothened Proteins
- 5 (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Genentech, Inc.
- (B) STREET: 460 Point San Bruno Blvd
- 10 (C) CITY: South San Francisco
- (D) STATE: California
- (E) COUNTRY: USA
- (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
- 15 (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- 20 (B) FILING DATE:
- (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Svoboda, Craig G.
- (B) REGISTRATION NUMBER: 39,044
- 25 (C) REFERENCE/DOCKET NUMBER: P1050PCT
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 415/225-1489
- (B) TELEFAX: 415/952-9881
- (C) TELEX: 910/371-7168
- 30 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3854 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- 35 (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- GCGGCGCGCT CGCGCGGAGG TGGCTGCTGG GCCGCGGGCT GGCCTGGGGG 50
- CGGAGCCGGG GAGCGACTCC CGCACCCAC GGCCGGTGCC TGCCCTCCAT 100
- CGAGGGGCTG GGAGTTAGTT TTAATGGTGG GAGAGGGAAT GGGGCTGAAG 150
- 40 ATCGGGGCCC CAGAGGGTTC CCAGGGTTGA AGACAATTCC AATCGAGGCG 200
- AGGGAGTCCG GGGTCCGTGC ATCCTGGCCC GGGCCTGCGC AGCTCAACAT 250

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   Pro Arg Arg Leu Leu Gln Leu Leu Leu Val Leu Leu
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   Gly Gly Arg Gly Arg Gly Ala Ala Leu Ser Gly Asn Val
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15  ACC GGG CCT GGG CCT CGC AGT GCC GGC GGG AGC GCG AGG 605
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     40             45             50

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   Arg Asn Ala Pro Val Thr Ser Pro Pro Pro Pro Leu Leu
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20  AGC CAC TGC GGC CGG GCC GCC CAC TGC GAG CCT TTG CGC 683
   Ser His Cys Gly Arg Ala Ala His Cys Glu Pro Leu Arg
           70             75

   TAC AAC GTG TGC CTG GGC TCC GCG CTG CCC TAC GGA GCC 722
   Tyr Asn Val Cys Leu Gly Ser Ala Leu Pro Tyr Gly Ala
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           135             140

   GAG TTG CCC AGC CGT ACC CTC TGC CAG GCC ACC CGA GGC 917
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   Pro Cys Ala Ile Val Glu Arg Glu Arg Gly Trp Pro Asp

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	Gln Cys Glu Ala Pro Leu Val Arg Thr Asp Asn Pro Lys		
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	Ser Trp Tyr Glu Asp Val Glu Gly Cys Gly Ile Gln Cys		
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	Val Asn Ala Cys Phe Phe Val Gly Ser Ile Gly Trp Leu		
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	GCC CAG TTC ATG GAT GGT GCC CGC CGG GAG ATT GTT TGC 1346		
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25 CTG GGC ATT TTT GGC TTC CTC GCC TTT GGC TTC GTG CTC 1853
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 30 Ile Thr Phe Ser Cys His Phe Tyr Asp Phe Phe Asn Gln
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30	Glu Ile Ser Pro Glu Leu Glu Lys Arg Leu Gly Arg Lys			
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	Ala Thr Ser Ala Val Pro Arg Leu Pro Gln Leu Pro Arg			
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 755 760 765

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 10 Arg Leu Gln Gly Leu Gly Ser Ile His Ser Arg Thr Asn
 770 775 780

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 15 Leu Met Glu Ala Glu Leu Leu Asp Ala Asp Ser Asp Phe
 785 790 793

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 CCATGTATCT GCCTACAAGA GCTGTGTACG ACTGGCTAGA AGCAGCCAGA 2980
 CCATAGAAAC AAGCTGAACA CAGCCACTGA TAGACCTCAC TTCAGAAGCA 3030
 20 AGACCTGCAG TTCAGGACCC TTGCCTCTGC CCCCCAATTA GAGTCTGGCT 3080
 GGCAGTGTTA GTCTCCAACA GAGCTTGTTAC TAGGGTAGGA ACGGCAGAGG 3130
 CAGGGGTGAT GGTACCCAGA GTGGGCTGGG GTGTCCAGTG AGGTAACCAA 3180
 GCCCATGTCT GGCAGATGAG GGCTGGCTGC CCTTTTCTGT GCCAATGAGT 3230
 GCCCTTTTCT GCGCTCTGA GACCAAAAGT GTTATTGTG TCATTTGTCC 3280
 25 TTTTCTAGG TGGGAACAGG ACTCTCTTTT TCCTCTTCCT GGTAGTTGTA 3330
 ATGACTACTC CCATAAGGCC TAGAACTGCT CTCAGTAGGT GGCCTGTCC 3380
 AAAACACATC TTCACATCTT AGTTCCACTA GGCCAAACTC TTATTGGTTA 3430
 GCACCTTAAA ACACACACAC ACACACACAC ACACACACAC ACACACACAC 3480
 ACACACACAC ACCCTCTTAC TTCTGAGCTT GGTCTCAAGA GAGAGACAAC 3530
 30 TGGTTCAGCT CCAGGCCTCT GAGAGTCATG TTTTCTTCCT CACATCCATC 3580
 CAGTGGGGAT GGATCCTCTG ACTTAAGGGG CTACCTTGGG AAGCCTCTGT 3630
 AGCTTCAGCC AGGCAAGAAA GCTTCTTCCA ACTTCTGTAT CTGGTGGGAA 3680
 GGAGGACTCC CTACTTTTTA CAATGTCTAG TCATTTTCAT AGTGCCCCAC 3730
 ATTCAAGAAC CAGACAGCAG GATGCCTTAG AAGCTGGCTG GGTTCAGGT 3780

CAGAGGCTCA GTATGAGAAG AAGAAATATG AACAGTAAAT AAAACATTTT 3830

TGTATAAAAA AAAAAAAAAA AAAA 3854

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 793 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

10	Met	Ala	Ala	Gly	Arg	Pro	Val	Arg	Gly	Pro	Glu	Leu	Ala	Pro	Arg	1	5	10	15
	Arg	Leu	Leu	Gln	Leu	Leu	Leu	Val	Leu	Leu	Gly	Gly	Arg	Gly		20	25	30	
	Arg	Gly	Ala	Ala	Leu	Ser	Gly	Asn	Val	Thr	Gly	Pro	Gly	Pro	Arg	35	40	45	
15	Ser	Ala	Gly	Gly	Ser	Ala	Arg	Arg	Asn	Ala	Pro	Val	Thr	Ser	Pro	50	55	60	
	Pro	Pro	Pro	Leu	Leu	Ser	His	Cys	Gly	Arg	Ala	Ala	His	Cys	Glu	65	70	75	
20	Pro	Leu	Arg	Tyr	Asn	Val	Cys	Leu	Gly	Ser	Ala	Leu	Pro	Tyr	Gly	80	85	90	
	Ala	Thr	Thr	Thr	Leu	Leu	Ala	Gly	Asp	Ser	Asp	Ser	Gln	Glu	Glu	95	100	105	
	Ala	His	Ser	Lys	Leu	Val	Leu	Trp	Ser	Gly	Leu	Arg	Asn	Ala	Pro	110	115	120	
25	Arg	Cys	Trp	Ala	Val	Ile	Gln	Pro	Leu	Leu	Cys	Ala	Val	Tyr	Met	125	130	135	
	Pro	Lys	Cys	Glu	Asn	Asp	Arg	Val	Glu	Leu	Pro	Ser	Arg	Thr	Leu	140	145	150	
30	Cys	Gln	Ala	Thr	Arg	Gly	Pro	Cys	Ala	Ile	Val	Glu	Arg	Glu	Arg	155	160	165	
	Gly	Trp	Pro	Asp	Phe	Leu	Arg	Cys	Thr	Pro	Asp	His	Phe	Pro	Glu	170	175	180	
	Gly	Cys	Pro	Asn	Glu	Val	Gln	Asn	Ile	Lys	Phe	Asn	Ser	Ser	Gly	185	190	195	
35	Gln	Cys	Glu	Ala	Pro	Leu	Val	Arg	Thr	Asp	Asn	Pro	Lys	Ser	Trp	200	205	210	
	Tyr	Glu	Asp	Val	Glu	Gly	Cys	Gly	Ile	Gln	Cys	Gln	Asn	Pro	Leu	215	220	225	

	Phe Thr Glu Ala Glu His Gln Asp Met His Ser Tyr Ile Ala Ala	230	235	240
	Phe Gly Ala Val Thr Gly Leu Cys Thr Leu Phe Thr Leu Ala Thr	245	250	255
5	Phe Val Ala Asp Trp Arg Asn Ser Asn Arg Tyr Pro Ala Val Ile	260	265	270
	Leu Phe Tyr Val Asn Ala Cys Phe Phe Val Gly Ser Ile Gly Trp	275	280	285
10	Leu Ala Gln Phe Met Asp Gly Ala Arg Arg Glu Ile Val Cys Arg	290	295	300
	Ala Asp Gly Thr Met Arg Phe Gly Glu Pro Thr Ser Ser Glu Thr	305	310	315
	Leu Ser Cys Val Ile Ile Phe Val Ile Val Tyr Tyr Ala Leu Met	320	325	330
15	Ala Gly Val Val Trp Phe Val Val Leu Thr Tyr Ala Trp His Thr	335	340	345
	Ser Phe Lys Ala Leu Gly Thr Thr Tyr Gln Pro Leu Ser Gly Lys	350	355	360
	Thr Ser Tyr Phe His Leu Leu Thr Trp Ser Leu Pro Phe Val Leu	365	370	375
20	Thr Val Ala Ile Leu Ala Val Ala Gln Val Asp Gly Asp Ser Val	380	385	390
	Ser Gly Ile Cys Phe Val Gly Tyr Lys Asn Tyr Arg Tyr Arg Ala	395	400	405
25	Gly Phe Val Leu Ala Pro Ile Gly Leu Val Leu Ile Val Gly Gly	410	415	420
	Tyr Phe Leu Ile Arg Gly Val Met Thr Leu Phe Ser Ile Lys Ser	425	430	435
	Asn His Pro Gly Leu Leu Ser Glu Lys Ala Ala Ser Lys Ile Asn	440	445	450
30	Glu Thr Met Leu Arg Leu Gly Ile Phe Gly Phe Leu Ala Phe Gly	455	460	465
	Phe Val Leu Ile Thr Phe Ser Cys His Phe Tyr Asp Phe Phe Asn	470	475	480
35	Gln Ala Glu Trp Glu Arg Ser Phe Arg Asp Tyr Val Leu Cys Gln	485	490	495
	Ala Asn Val Thr Ile Gly Leu Pro Thr Lys Lys Pro Ile Pro Asp	500	505	510
	Cys Glu Ile Lys Asn Arg Pro Ser Leu Leu Val Glu Lys Ile Asn			

	515	520	525
	Leu Phe Ala Met Phe Gly Thr Gly Ile Ala Met Ser Thr Trp Val		
	530	535	540
5	Trp Thr Lys Ala Thr Leu Leu Ile Trp Arg Arg Thr Trp Cys Arg		
	545	550	555
	Leu Thr Gly His Ser Asp Asp Glu Pro Lys Arg Ile Lys Lys Ser		
	560	565	570
	Lys Met Ile Ala Lys Ala Phe Ser Lys Arg Arg Glu Leu Leu Gln		
	575	580	585
10	Asn Pro Gly Gln Glu Leu Ser Phe Ser Met His Thr Val Ser His		
	590	595	600
	Asp Gly Pro Val Ala Gly Leu Ala Phe Glu Leu Asn Glu Pro Ser		
	605	610	615
15	Ala Asp Val Ser Ser Ala Trp Ala Gln His Val Thr Lys Met Val		
	620	625	630
	Ala Arg Arg Gly Ala Ile Leu Pro Gln Asp Val Ser Val Thr Pro		
	635	640	645
	Val Ala Thr Pro Val Pro Pro Glu Glu Gln Ala Asn Leu Trp Leu		
	650	655	660
20	Val Glu Ala Glu Ile Ser Pro Glu Leu Glu Lys Arg Leu Gly Arg		
	665	670	675
	Lys Lys Lys Arg Arg Lys Arg Lys Lys Glu Val Cys Pro Leu Gly		
	680	685	690
25	Pro Ala Pro Glu Leu His His Ser Ala Pro Val Pro Ala Thr Ser		
	695	700	705
	Ala Val Pro Arg Leu Pro Gln Leu Pro Arg Gln Lys Cys Leu Val		
	710	715	720
	Ala Ala Asn Ala Trp Gly Thr Gly Glu Pro Cys Arg Gln Gly Ala		
	725	730	735
30	Trp Thr Val Val Ser Asn Pro Phe Cys Pro Glu Pro Ser Pro His		
	740	745	750
	Gln Asp Pro Phe Leu Pro Gly Ala Ser Ala Pro Arg Val Trp Ala		
	755	760	765
35	Gln Gly Arg Leu Gln Gly Leu Gly Ser Ile His Ser Arg Thr Asn		
	770	775	780
	Leu Met Glu Ala Glu Leu Leu Asp Ala Asp Ser Asp Phe		
	785	790	793

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2972 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

5 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGGGGTTGG CC ATG GCC GCT GCC CGC CCA GCG CGG GGG 39
Met Ala Ala Ala Arg Pro Ala Arg Gly
1 5

10 CCG GAG CTC CCG CTC CTG GGG CTG CTG CTG CTG CTG 78
Pro Glu Leu Pro Leu Leu Gly Leu Leu Leu Leu Leu
10 15 20

CTG GGG GAC CCG GGC CGG GGG GCG GCC TCG AGC GGG AAC 117
Leu Gly Asp Pro Gly Arg Gly Ala Ala Ser Ser Gly Asn
15 25 30 35

GCG ACC GGG CCT GGG CCT CGG AGC GCG GGC GGG AGC GCG 156
Ala Thr Gly Pro Gly Pro Arg Ser Ala Gly Gly Ser Ala
40 45

20 AGG AGG AGC GCG GCG GTG ACT GGC CCT CCG CCG CCG CTG 195
Arg Arg Ser Ala Ala Val Thr Gly Pro Pro Pro Pro Leu
50 55 60

AGC CAC TGC GGC CGG GCT GCC CCC TGC GAG CCG CTG CGC 234
Ser His Cys Gly Arg Ala Ala Pro Cys Glu Pro Leu Arg
65 70

25 TAC AAC GTG TGC CTG GGC TCG GTG CTG CCC TAC GGG GCC 273
Tyr Asn Val Cys Leu Gly Ser Val Leu Pro Tyr Gly Ala
75 80 85

ACC TCC ACA CTG CTG GCC GGA GAC TCG GAC TCC CAG GAG 312
Thr Ser Thr Leu Leu Ala Gly Asp Ser Asp Ser Gln Glu
30 90 95 100

GAA GCG CAC GGC AAG CTC GTG CTC TGG TCG GGC CTC CGG 351
Glu Ala His Gly Lys Leu Val Leu Trp Ser Gly Leu Arg
105 110

35 AAT GCC CCC CGC TGC TGG GCA GTG ATC CAG CCC CTG CTG 390
Asn Ala Pro Arg Cys Trp Ala Val Ile Gln Pro Leu Leu
115 120 125

TGT GCC GTA TAC ATG CCC AAG TGT GAG AAT GAC CGG GTG 429
Cys Ala Val Tyr Met Pro Lys Cys Glu Asn Asp Arg Val
130 135

40 GAG CTG CCC AGC CGT ACC CTC TGC CAG GCC ACC CGA GGC 468
Glu Leu Pro Ser Arg Thr Leu Cys Gln Ala Thr Arg Gly
140 145 150

CCC TGT GCC ATC GTG GAG AGG GAG CGG GGC TGG CCT GAC 507
Pro Cys Ala Ile Val Glu Arg Glu Arg Gly Trp Pro Asp

	155	160	165	
	TTC CTG CGC TGC ACT CCT GAC CGC TTC CCT GAA GGC TGC			546
	Phe Leu Arg Cys Thr Pro Asp Arg Phe Pro Glu Gly Cys			
	170	175		
5	ACG AAT GAG GTG CAG AAC ATC AAG TTC AAC AGT TCA GGC			585
	Thr Asn Glu Val Gln Asn Ile Lys Phe Asn Ser Ser Gly			
	180	185	190	
	CAG TGC GAA GTG CCC TTG GTT CGG ACA GAC AAC CCC AAG			624
	Gln Cys Glu Val Pro Leu Val Arg Thr Asp Asn Pro Lys			
10	195	200		
	AGC TGG TAC GAG GAC GTG GAG GGC TGC GGC ATC CAG TGC			663
	Ser Trp Tyr Glu Asp Val Glu Gly Cys Gly Ile Gln Cys			
	205	210	215	
	CAG AAC CCG CTC TTC ACA GAG GCT GAG CAC CAG GAC ATG			702
15	Gln Asn Pro Leu Phe Thr Glu Ala Glu His Gln Asp Met			
	220	225	230	
	CAC AGC TAC ATC GCG GCC TTC GGG GCC GTC ACG GGC CTC			741
	His Ser Tyr Ile Ala Ala Phe Gly Ala Val Thr Gly Leu			
	235	240		
20	TGC ACG CTC TTC ACC CTG GCC ACA TTC GTG GCT GAC TGG			780
	Cys Thr Leu Phe Thr Leu Ala Thr Phe Val Ala Asp Trp			
	245	250	255	
	CGG AAC TCG AAT CGC TAC CCT GCT GTT ATT CTC TTC TAC			819
25	Arg Asn Ser Asn Arg Tyr Pro Ala Val Ile Leu Phe Tyr			
	260	265		
	GTC AAT GCG TGC TTC TTT GTG GGC AGC ATT GGC TGG CTG			858
	Val Asn Ala Cys Phe Phe Val Gly Ser Ile Gly Trp Leu			
	270	275	280	
	GCC CAG TTC ATG GAT GGT GCC CGC CGA GAG ATC GTC TGC			897
30	Ala Gln Phe Met Asp Gly Ala Arg Arg Glu Ile Val Cys			
	285	290	295	
	CGT GCA GAT GGC ACC ATG AGG CTT GGG GAG CCC ACC TCC			936
	Arg Ala Asp Gly Thr Met Arg Leu Gly Glu Pro Thr Ser			
	300	305		
35	AAT GAG ACT CTG TCC TGC GTC ATC ATC TTT GTC ATC GTG			975
	Asn Glu Thr Leu Ser Cys Val Ile Ile Phe Val Ile Val			
	310	315	320	
	TAC TAC GCC CTG ATG GCT GGT GTG GTT TGG TTT GTG GTC			1014
	Tyr Tyr Ala Leu Met Ala Gly Val Val Trp Phe Val Val			
40	325	330		
	CTC ACC TAT GCC TGG CAC ACT TCC TTC AAA GCC CTG GGC			1053
	Leu Thr Tyr Ala Trp His Thr Ser Phe Lys Ala Leu Gly			
	335	340	345	

ACC ACC TAC CAG CCT CTC TCG GGC AAG ACC TCC TAC TTC 1092
 Thr Thr Tyr Gln Pro Leu Ser Gly Lys Thr Ser Tyr Phe
 350 355 360

CAC CTG CTC ACC TGG TCA CTC CCC TTT GTC CTC ACT GTG 1131
 5 His Leu Leu Thr Trp Ser Leu Pro Phe Val Leu Thr Val
 365 370

GCA ATC CTT GCT GTG GCG CAG GTG GAT GGG GAC TCT GTG 1170
 Ala Ile Leu Ala Val Ala Gln Val Asp Gly Asp Ser Val
 375 380 385

10 AGT GGC ATT TGT TTT GTG GGC TAC AAG AAC TAC CGA TAC 1209
 Ser Gly Ile Cys Phe Val Gly Tyr Lys Asn Tyr Arg Tyr
 390 395

CGT GCG GGC TTC GTG CTG GCC CCA ATC GGC CTG GTG CTC 1248
 Arg Ala Gly Phe Val Leu Ala Pro Ile Gly Leu Val Leu
 15 400 405 410

ATC GTG GGA GGC TAC TTC CTC ATC CGA GGA GTC ATG ACT 1287
 Ile Val Gly Gly Tyr Phe Leu Ile Arg Gly Val Met Thr
 415 420 425

CTG TTC TCC ATC AAG AGC AAC CAC CCC GGG CTG CTG AGT 1326
 20 Leu Phe Ser Ile Lys Ser Asn His Pro Gly Leu Leu Ser
 430 435

GAG AAG GCT GCC AGC AAG ATC AAC GAG ACC ATG CTG CGC 1365
 Glu Lys Ala Ala Ser Lys Ile Asn Glu Thr Met Leu Arg
 440 445 450

25 CTG GGC ATT TTT GGC TTC CTG GCC TTT GGC TTT GTG CTC 1404
 Leu Gly Ile Phe Gly Phe Leu Ala Phe Gly Phe Val Leu
 455 460

ATT ACC TTC AGC TGC CAC TTC TAC GAC TTC TTC AAC CAG 1443
 30 Ile Thr Phe Ser Cys His Phe Tyr Asp Phe Phe Asn Gln
 465 470 475

GCT GAG TGG GAG CGC AGC TTC CGG GAC TAT GTG CTA TGT 1482
 Ala Glu Trp Glu Arg Ser Phe Arg Asp Tyr Val Leu Cys
 480 485 490

CAG GCC AAT GTG ACC ATC GGG CTG CCC ACC AAG CAG CCC 1521
 35 Gln Ala Asn Val Thr Ile Gly Leu Pro Thr Lys Gln Pro
 495 500

ATC CCT GAC TGT GAG ATC AAG AAT CGC CCG AGC CTT CTG 1560
 Ile Pro Asp Cys Glu Ile Lys Asn Arg Pro Ser Leu Leu
 505 510 515

40 GTG GAG AAG ATC AAC CTG TTT GCC ATG TTT GGA ACT GGC 1599
 Val Glu Lys Ile Asn Leu Phe Ala Met Phe Gly Thr Gly
 520 525

ATC GCC ATG AGC ACC TGG GTC TGG ACC AAG GCC ACG CTG 1638
 Ile Ala Met Ser Thr Trp Val Trp Thr Lys Ala Thr Leu

	530		535		540	
	CTC ATC TGG AGG CGT ACC TGG TGC AGG TTG ACT GGG CAG 1677					
	Leu Ile Trp Arg Arg Thr Trp Cys Arg Leu Thr Gly Gln					
	545		550		555	
5	AGT GAC GAT GAG CCA AAG CGG ATC AAG AAG AGC AAG ATG 1716					
	Ser Asp Asp Glu Pro Lys Arg Ile Lys Lys Ser Lys Met					
	560		565			
	ATT GCC AAG GCC TTC TCT AAG CGG CAC GAG CTC CTG CAG 1755					
	Ile Ala Lys Ala Phe Ser Lys Arg His Glu Leu Leu Gln					
10	570		575		580	
	AAC CCA GGC CAG GAG CTG TCC TTC AGC ATG CAC ACT GTG 1794					
	Asn Pro Gly Gln Glu Leu Ser Phe Ser Met His Thr Val					
	585		590			
	TCC CAC GAC GGG CCC GTG GCG GGC TTG GCC TTT GAC CTC 1833					
15	Ser His Asp Gly Pro Val Ala Gly Leu Ala Phe Asp Leu					
	595		600		605	
	AAT GAG CCC TCA GCT GAT GTC TCC TCT GCC TGG GCC CAG 1872					
	Asn Glu Pro Ser Ala Asp Val Ser Ser Ala Trp Ala Gln					
	610		615		620	
20	CAT GTC ACC AAG ATG GTG GCT CGG AGA GGA GCC ATA CTG 1911					
	His Val Thr Lys Met Val Ala Arg Arg Gly Ala Ile Leu					
	625		630			
	CCC CAG GAT ATT TCT GTC ACC CCT GTG GCA ACT CCA GTG 1950					
	Pro Gln Asp Ile Ser Val Thr Pro Val Ala Thr Pro Val					
25	635		640		645	
	CCC CCA GAG GAA CAA GCC AAC CTG TGG CTG GTT GAG GCA 1989					
	Pro Pro Glu Glu Gln Ala Asn Leu Trp Leu Val Glu Ala					
	650		655			
	GAG ATC TCC CCA GAG CTG CAG AAG CGC CTG GGC CGG AAG 2028					
30	Glu Ile Ser Pro Glu Leu Gln Lys Arg Leu Gly Arg Lys					
	660		665		670	
	AAG AAG AGG AGG AAG AGG AAG AAG GAG GTG TGC CCG CTG 2067					
	Lys Lys Arg Arg Lys Arg Lys Lys Glu Val Cys Pro Leu					
	675		680		685	
35	GCG CCG CCC CCT GAG CTT CAC CCC CCT GCC CCT GCC CCC 2106					
	Ala Pro Pro Pro Glu Leu His Pro Pro Ala Pro Ala Pro					
	690		695			
	AGT ACC ATT CCT CGA CTG CCT CAG CTG CCC CGG CAG AAA 2145					
	Ser Thr Ile Pro Arg Leu Pro Gln Leu Pro Arg Gln Lys					
40	700		705		710	
	TGC CTG GTG GCT GCA GGT GCC TGG GGA GCT GGG GAC TCT 2184					
	Cys Leu Val Ala Ala Gly Ala Trp Gly Ala Gly Asp Ser					
	715		720			

TGC CGA CAG GGA GCG TGG ACC CTG GTC TCC AAC CCA TTC 2223
 Cys Arg Gln Gly Ala Trp Thr Leu Val Ser Asn Pro Phe
 725 730 735

5 TGC CCA GAG CCC AGT CCC CCT CAG GAT CCA TTT CTG CCC 2262
 Cys Pro Glu Pro Ser Pro Pro Gln Asp Pro Phe Leu Pro
 740 745 750

AGT GCA CCG GCC CCC GTG GCA TGG GCT CAT GGC CGC CGA 2301
 Ser Ala Pro Ala Pro Val Ala Trp Ala His Gly Arg Arg
 755 760

10 CAG GGC CTG GGG CCT ATT CAC TCC CGC ACC AAC CTG ATG 2340
 Gln Gly Leu Gly Pro Ile His Ser Arg Thr Asn Leu Met
 765 770 775

GAC ACA GAA CTC ATG GAT GCA GAC TCG GAC TTC TGAGCCT 2380
 Asp Thr Glu Leu Met Asp Ala Asp Ser Asp Phe
 15 780 785 787

GCAGAGCAGG ACCTGGGACA GGAAAGAGAG GAACCAATAC CTTCAAGGCT 2430
 CTTCTTCCTC ACCGAGCATG CTTCCTTAGG ATCCCGTCTT CCAGAGAACC 2480
 TGTGGGCTGA CTGCCCTCCG AAGAGAGTTC TGGATGTCTG GCTCAAAGCA 2530
 GCAGGACTGT GGGAAAGAGC CTAACATCTC CATGGGGAGG CCTCACCCCA 2580
 20 GGGACAGGGC CCTGGAGCTC AGGGTCCTTG TTTCTGCCCT GCCAGCTGCA 2630
 GCCTGGTTGG CAGCATCTGC TCCATCGGGG CAGGGGGTAT GCAGAGCTTG 2680
 TGGTGGGGCA GGAACGGTGG AGGCAGAGGT GACAGTTCCC AGAGTGGGCT 2730
 TTGGTGGCCA GGGAGGCAGC CTAGCCTATG TCTGGCAGAT GAGGGCTGGC 2780
 TGCCGTTTTT TGGGCTGATG GGTGCCCTTT CCTGGCAGTC TCAGTCCAAA 2830
 25 AGTGTGACT GTGTCATTAG TCCTTTGTCT AAGTAGGGCC AGGGCACCGT 2880
 ATTCCTCTCC CAGGTGTTTG TGGGGCTGGA AGGACCTGCT CCCACAGGGG 2930
 CCATGTCCTC TCTTAATAGG TGGCACTACC CCAAACCCAC CG 2972

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 787 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

35 Met Ala Ala Ala Arg Pro Ala Arg Gly Pro Glu Leu Pro Leu Leu
 1 5 10 15
 Gly Leu Leu Leu Leu Leu Leu Gly Asp Pro Gly Arg Gly Ala
 20 25 30

	Ala Ser Ser Gly Asn Ala Thr Gly Pro Gly Pro Arg Ser Ala Gly	35	40	45
	Gly Ser Ala Arg Arg Ser Ala Ala Val Thr Gly Pro Pro Pro Pro	50	55	60
5	Leu Ser His Cys Gly Arg Ala Ala Pro Cys Glu Pro Leu Arg Tyr	65	70	75
	Asn Val Cys Leu Gly Ser Val Leu Pro Tyr Gly Ala Thr Ser Thr	80	85	90
10	Leu Leu Ala Gly Asp Ser Asp Ser Gln Glu Glu Ala His Gly Lys	95	100	105
	Leu Val Leu Trp Ser Gly Leu Arg Asn Ala Pro Arg Cys Trp Ala	110	115	120
	Val Ile Gln Pro Leu Leu Cys Ala Val Tyr Met Pro Lys Cys Glu	125	130	135
15	Asn Asp Arg Val Glu Leu Pro Ser Arg Thr Leu Cys Gln Ala Thr	140	145	150
	Arg Gly Pro Cys Ala Ile Val Glu Arg Glu Arg Gly Trp Pro Asp	155	160	165
20	Phe Leu Arg Cys Thr Pro Asp Arg Phe Pro Glu Gly Cys Thr Asn	170	175	180
	Glu Val Gln Asn Ile Lys Phe Asn Ser Ser Gly Gln Cys Glu Val	185	190	195
	Pro Leu Val Arg Thr Asp Asn Pro Lys Ser Trp Tyr Glu Asp Val	200	205	210
25	Glu Gly Cys Gly Ile Gln Cys Gln Asn Pro Leu Phe Thr Glu Ala	215	220	225
	Glu His Gln Asp Met His Ser Tyr Ile Ala Ala Phe Gly Ala Val	230	235	240
30	Thr Gly Leu Cys Thr Leu Phe Thr Leu Ala Thr Phe Val Ala Asp	245	250	255
	Trp Arg Asn Ser Asn Arg Tyr Pro Ala Val Ile Leu Phe Tyr Val	260	265	270
	Asn Ala Cys Phe Phe Val Gly Ser Ile Gly Trp Leu Ala Gln Phe	275	280	285
35	Met Asp Gly Ala Arg Arg Glu Ile Val Cys Arg Ala Asp Gly Thr	290	295	300
	Met Arg Leu Gly Glu Pro Thr Ser Asn Glu Thr Leu Ser Cys Val	305	310	315
	Ile Ile Phe Val Ile Val Tyr Tyr Ala Leu Met Ala Gly Val Val			

		320		325		330
	Trp Phe Val Val	Leu Thr Tyr Ala Trp	His Thr Ser Phe Lys Ala			
		335		340		345
5	Leu Gly Thr Thr	Tyr Gln Pro Leu Ser	Gly Lys Thr Ser Tyr Phe			
		350		355		360
	His Leu Leu Thr	Trp Ser Leu Pro Phe	Val Leu Thr Val Ala Ile			
		365		370		375
	Leu Ala Val Ala	Gln Val Asp Gly Asp	Ser Val Ser Gly Ile Cys			
		380		385		390
10	Phe Val Gly Tyr	Lys Asn Tyr Arg Tyr	Arg Ala Gly Phe Val Leu			
		395		400		405
	Ala Pro Ile Gly	Leu Val Leu Ile Val	Gly Gly Tyr Phe Leu Ile			
		410		415		420
15	Arg Gly Val Met	Thr Leu Phe Ser Ile	Lys Ser Asn His Pro Gly			
		425		430		435
	Leu Leu Ser Glu	Lys Ala Ala Ser Lys	Ile Asn Glu Thr Met Leu			
		440		445		450
	Arg Leu Gly Ile	Phe Gly Phe Leu Ala	Phe Gly Phe Val Leu Ile			
		455		460		465
20	Thr Phe Ser Cys	His Phe Tyr Asp Phe	Phe Asn Gln Ala Glu Trp			
		470		475		480
	Glu Arg Ser Phe	Arg Asp Tyr Val Leu	Cys Gln Ala Asn Val Thr			
		485		490		495
25	Ile Gly Leu Pro	Thr Lys Gln Pro Ile	Pro Asp Cys Glu Ile Lys			
		500		505		510
	Asn Arg Pro Ser	Leu Leu Val Glu Lys	Ile Asn Leu Phe Ala Met			
		515		520		525
	Phe Gly Thr Gly	Ile Ala Met Ser Thr	Trp Val Trp Thr Lys Ala			
		530		535		540
30	Thr Leu Leu Ile	Trp Arg Arg Thr Trp	Cys Arg Leu Thr Gly Gln			
		545		550		555
	Ser Asp Asp Glu	Pro Lys Arg Ile Lys	Lys Ser Lys Met Ile Ala			
		560		565		570
35	Lys Ala Phe Ser	Lys Arg His Glu Leu	Leu Gln Asn Pro Gly Gln			
		575		580		585
	Glu Leu Ser Phe	Ser Met His Thr Val	Ser His Asp Gly Pro Val			
		590		595		600
	Ala Gly Leu Ala	Phe Asp Leu Asn Glu	Pro Ser Ala Asp Val Ser			
		605		610		615

	Ser	Ala	Trp	Ala	Gln	His	Val	Thr	Lys	Met	Val	Ala	Arg	Arg	Gly	
					620					625					630	
	Ala	Ile	Leu	Pro	Gln	Asp	Ile	Ser	Val	Thr	Pro	Val	Ala	Thr	Pro	
					635					640					645	
5	Val	Pro	Pro	Glu	Glu	Gln	Ala	Asn	Leu	Trp	Leu	Val	Glu	Ala	Glu	
					650					655					660	
	Ile	Ser	Pro	Glu	Leu	Gln	Lys	Arg	Leu	Gly	Arg	Lys	Lys	Lys	Arg	
					665					670					675	
10	Arg	Lys	Arg	Lys	Lys	Glu	Val	Cys	Pro	Leu	Ala	Pro	Pro	Pro	Glu	
					680					685					690	
	Leu	His	Pro	Pro	Ala	Pro	Ala	Pro	Ser	Thr	Ile	Pro	Arg	Leu	Pro	
					695					700					705	
	Gln	Leu	Pro	Arg	Gln	Lys	Cys	Leu	Val	Ala	Ala	Gly	Ala	Trp	Gly	
					710					715					720	
15	Ala	Gly	Asp	Ser	Cys	Arg	Gln	Gly	Ala	Trp	Thr	Leu	Val	Ser	Asn	
					725					730					735	
	Pro	Phe	Cys	Pro	Glu	Pro	Ser	Pro	Pro	Gln	Asp	Pro	Phe	Leu	Pro	
					740					745					750	
20	Ser	Ala	Pro	Ala	Pro	Val	Ala	Trp	Ala	His	Gly	Arg	Arg	Gln	Gly	
					755					760					765	
	Leu	Gly	Pro	Ile	His	Ser	Arg	Thr	Asn	Leu	Met	Asp	Thr	Glu	Leu	
					770					775					780	
	Met	Asp	Ala	Asp	Ser	Asp	Phe									
					785		787									

WHAT IS CLAIMED IS:

1. Isolated vertebrate Smoothened.
2. Isolated vertebrate Smoothened having at least about 80% sequence identity with native sequence vertebrate Smoothened comprising amino acid residues 1 to 787 of SEQ ID NO:4.
- 5 3. The vertebrate Smoothened of claim 2 wherein said Smoothened has at least about 90% sequence identity.
4. The vertebrate Smoothened of claim 3 wherein said Smoothened has at least about 95% sequence identity.
5. Isolated native sequence vertebrate Smoothened comprising the amino acid sequence of SEQ
10 ID NO:4.
6. Isolated native sequence vertebrate Smoothened comprising the amino acid sequence of SEQ ID NO:2.
7. A chimeric molecule comprising the vertebrate Smoothened of claim 1 fused to a heterologous amino acid sequence.
- 15 8. The chimeric molecule of claim 7 wherein said heterologous amino acid sequence is an epitope tag sequence.
9. An antibody which specifically binds to the vertebrate Smoothened of claim 1.
10. The antibody of claim 9 wherein said antibody is a monoclonal antibody.
11. The antibody of claim 9 which is a neutralizing antibody.
- 20 12. The antibody of claim 9 which is an agonist antibody.
13. Isolated nucleic acid encoding vertebrate Smoothened.
14. The nucleic acid of claim 13 wherein said nucleic acid encodes native sequence vertebrate Smoothened comprising the amino acid sequence of SEQ ID NO:4.
15. The nucleic acid of claim 13 wherein said nucleic acid encodes native sequence vertebrate
25 Smoothened comprising the amino acid sequence of SEQ ID NO:2.
16. A vector comprising the nucleic acid of claim 13.
17. The vector of claim 16 operably linked to control sequences recognized by a host cell transformed with the vector.
18. A host cell comprising the vector of claim 16.
- 30 19. A process of using a nucleic acid molecule encoding vertebrate Smoothened to effect production of vertebrate Smoothened comprising culturing the host cell of claim 18.
20. The process of claim 19 further comprising recovering the vertebrate Smoothened from the host cell culture.
21. An article of manufacture, comprising a container and a composition contained within said
35 container, wherein the composition includes vertebrate Smoothened or vertebrate Smoothened antibodies.
22. The article of manufacture of claim 21 further comprising instructions for using the vertebrate Smoothened or vertebrate Smoothened antibodies *in vivo* or *ex vivo*.
23. A non-human, transgenic animal which contains cells that express nucleic acid encoding vertebrate Smoothened.

24. The animal of claim 23 which is a mouse or rat.
25. A non-human, knockout animal which contains cells having an altered gene encoding vertebrate Smoothed.
- 5 26. The animal of claim 25 which is a mouse or rat.
27. A protein complex comprising vertebrate Smoothed protein and vertebrate Patched protein.
28. The protein complex of claim 27 further comprising vertebrate Hedgehog protein.
29. The protein complex of claim 28 wherein the vertebrate Hedgehog protein binds to the vertebrate Patched protein but does not bind to the vertebrate Smoothed protein.
30. The protein complex of claim 27 which is a receptor for vertebrate Hedgehog protein.
- 10 31. A vertebrate Patched which binds to vertebrate Smoothed.
32. The vertebrate Patched of claim 31 which has less than 100% sequence identity with a native sequence vertebrate Patched.

1/24

GCGGCGCGCT CGCGCGGAGG TGGCTGCTGG GCCGCGGGCT GGCCTGGGGG 50
 CGGAGCCGGG GAGCGACTCC CGCACCCAC GGCCGGTGCC TGCCCTCCAT 100
 CGAGGGGCTG GGAGTTAGTT TTAATGGTGG GAGAGGGAAT GGGGCTGAAG 150
 ATCGGGGCCC CAGAGGGTTC CCAGGGTTGA AGACAATTCC AATCGAGGCG 200
 AGGGAGTCCG GGGTCCGTGC ATCCTGGCCC GGGCCTGCGC AGCTCAACAT 250
 GGGGCCCCGGG TTCCAAAGTT TGCAAAGTTG GGAGCCGAGG GGCCCGGACG 300
 CGCGCGGCGC CTGGCGAAAG CTGGCCCCAG ACTTTCGGGG CGCACCGGTC 350
 GCCTAAGTAG CCTCCGCGGC CCCCAGGGTC GTGTGTGTGG CCAGGGGACT 400
 CCGGGGAGCT CCGGGGCGCC TCAGCTTCTG CTGAGTTGGC GGTTTGGCC 449

 ATG GCT GCT GGC CGC CCC GTG CGT GGG CCC GAG CTG GCG 488
 Met Ala Ala Gly Arg Pro Val Arg Gly Pro Glu Leu Ala
 1 5 10

 CCC CGG AGG CTG CTG CAG TTG CTG CTG CTG GTA CTG CTT 527
 Pro Arg Arg Leu Leu Gln Leu Leu Leu Leu Val Leu Leu
 15 20 25

 GGG GGC CGG GGC CGG GGG GCG GCC TTG AGC GGG AAC GTG 566
 Gly Gly Arg Gly Arg Gly Ala Ala Leu Ser Gly Asn Val
 30 35

 ACC GGG CCT GGG CCT CGC AGT GCC GGC GGG AGC GCG AGG 605
 Thr Gly Pro Gly Pro Arg Ser Ala Gly Gly Ser Ala Arg
 40 45 50

 AGG AAC GCG CCG GTG ACC AGC CCT CCG CCG CCG CTG CTG 644
 Arg Asn Ala Pro Val Thr Ser Pro Pro Pro Pro Leu Leu
 55 60 65

 AGC CAC TGC GGC CGG GCC GCC CAC TGC GAG CCT TTG CGC 683
 Ser His Cys Gly Arg Ala Ala His Cys Glu Pro Leu Arg
 70 75

 TAC AAC GTG TGC CTG GGC TCC GCG CTG CCC TAC GGA GCC 722
 Tyr Asn Val Cys Leu Gly Ser Ala Leu Pro Tyr Gly Ala
 80 85 90

 ACC ACC ACG CTG CTG GCT GGG GAC TCG GAC TCG CAG GAG 761
 Thr Thr Thr Leu Leu Ala Gly Asp Ser Asp Ser Gln Glu
 95 100

 GAA GCG CAC AGC AAG CTC GTG CTC TGG TCC GGC CTC CGG 800
 Glu Ala His Ser Lys Leu Val Leu Trp Ser Gly Leu Arg
 105 110 115

FIG. 1A

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2/24

AAT	GCT	CCC	CGA	TGC	TGG	GCA	GTG	ATC	CAG	CCC	CTG	CTG	839
Asn	Ala	Pro	Arg	Cys	Trp	Ala	Val	Ile	Gln	Pro	Leu	Leu	
		120					125					130	
TGT	GCT	GTC	TAC	ATG	CCC	AAG	TGT	GAA	AAT	GAC	CGA	GTG	878
Cys	Ala	Val	Tyr	Met	Pro	Lys	Cys	Glu	Asn	Asp	Arg	Val	
				135					140				
GAG	TTG	CCC	AGC	CGT	ACC	CTC	TGC	CAG	GCC	ACC	CGA	GGC	917
Glu	Leu	Pro	Ser	Arg	Thr	Leu	Cys	Gln	Ala	Thr	Arg	Gly	
	145					150					155		
CCC	TGT	GCC	ATT	GTG	GAG	CGG	GAA	CGA	GGG	TGG	CCT	GAC	956
Pro	Cys	Ala	Ile	Val	Glu	Arg	Glu	Arg	Gly	Trp	Pro	Asp	
			160					165					
TTT	CTG	CGT	TGC	ACG	CCG	GAC	CAC	TTC	CCT	GAA	GGC	TGT	995
Phe	Leu	Arg	Cys	Thr	Pro	Asp	His	Phe	Pro	Glu	Gly	Cys	
170					175					180			
CCA	AAC	GAG	GTA	CAA	AAC	ATC	AAG	TTC	AAC	AGT	TCA	GGC	1034
Pro	Asn	Glu	Val	Gln	Asn	Ile	Lys	Phe	Asn	Ser	Ser	Gly	
		185					190					195	
CAA	TGT	GAA	GCA	CCC	TTG	GTG	AGG	ACA	GAC	AAC	CCC	AAG	1073
Gln	Cys	Glu	Ala	Pro	Leu	Val	Arg	Thr	Asp	Asn	Pro	Lys	
				200					205				
AGC	TGG	TAC	GAG	GAC	GTG	GAG	GGC	TGT	GGG	ATC	CAG	TGC	1112
Ser	Trp	Tyr	Glu	Asp	Val	Glu	Gly	Cys	Gly	Ile	Gln	Cys	
	210					215					220		
CAG	AAC	CCG	CTG	TTC	ACC	GAG	GCT	GAG	CAC	CAG	GAC	ATG	1151
Gln	Asn	Pro	Leu	Phe	Thr	Glu	Ala	Glu	His	Gln	Asp	Met	
			225				230						
CAC	AGT	TAC	ATC	GCA	GCC	TTC	GGG	GCG	GTC	ACC	GGC	CTC	1190
His	Ser	Tyr	Ile	Ala	Ala	Phe	Gly	Ala	Val	Thr	Gly	Leu	
235					240					245			
TGT	ACA	CTC	TTC	ACC	CTG	GCC	ACC	TTT	GTG	GCT	GAC	TGG	1229
Cys	Thr	Leu	Phe	Thr	Leu	Ala	Thr	Phe	Val	Ala	Asp	Trp	
		250					255					260	
CGG	AAC	TCC	AAT	CGC	TAC	CCT	GCG	GTT	ATT	CTC	TTC	TAT	1268
Arg	Asn	Ser	Asn	Arg	Tyr	Pro	Ala	Val	Ile	Leu	Phe	Tyr	
			265					270					
GTC	AAT	GCG	TGT	TTC	TTT	GTG	GGC	AGC	ATT	GGC	TGG	CTG	1307
Val	Asn	Ala	Cys	Phe	Phe	Val	Gly	Ser	Ile	Gly	Trp	Leu	
	275					280					285		

FIG. 1B

3/24

TAC TAT GCC TTG ATG GCT GGA GTA GTG TGG TTC GTG GTC 1463
 Tyr Tyr Ala Leu Met Ala Gly Val Val Trp Phe Val Val
 330 335

CTC ACC TAT GCC TGG CAC ACC TCC TTC AAA GCC CTG GGC 1502
 Leu Thr Tyr Ala Trp His Thr Ser Phe Lys Ala Leu Gly
 340 345 350

ACC ACT TAC CAG CCT CTC TCG GGC AAG ACA TCC TAT TTC 1541
 Thr Thr Tyr Gln Pro Leu Ser Gly Lys Thr Ser Tyr Phe
 355 360

CAC CTG CTC ACG TGG TCA CTC CCC TTC GTC CTC ACT GTG 1580
 His Leu Leu Thr Trp Ser Leu Pro Phe Val Leu Thr Val
 365 370 375

GCA ATC CTT GCT GTG GCT CAG GTA GAT GGG GAC TCC GTG 1619
 Ala Ile Leu Ala Val Ala Gln Val Asp Gly Asp Ser Val
 380 385 390

AGT GGC ATC TGC TTT GTA GGC TAC AAG AAC TAT CGG TAC 1658
 Ser Gly Ile Cys Phe Val Gly Tyr Lys Asn Tyr Arg Tyr
 395 400

CGT GCT GGC TTT GTA CTT GCC CCA ATT GGC CTG GTG CTT 1697
 Arg Ala Gly Phe Val Leu Ala Pro Ile Gly Leu Val Leu
 405 410 415

ATT GTG GGA GGC TAC TTC CTC ATC CGA GGG GTC ATG ACT 1736
 Ile Val Gly Gly Tyr Phe Leu Ile Arg Gly Val Met Thr
 420 425

CTG TTC TCC ATC AAG AGC AAC CAC CCT GGG CTT CTG AGT 1775
 Leu Phe Ser Ile Lys Ser Asn His Pro Gly Leu Leu Ser
 430 435 440

GAG AAG GCA GCC AGC AAG ATC AAT GAG ACC ATG CTG CGC 1814
 Glu Lys Ala Ala Ser Lys Ile Asn Glu Thr Met Leu Arg
 445 450 455

CTG GGC ATT TTT GGC TTC CTC GCC TTT GGC TTC GTG CTC 1853
 Leu Gly Ile Phe Gly Phe Leu Ala Phe Gly Phe Val Leu
 460 465

ATC ACC TTC AGC TGC CAC TTC TAT GAC TTC TTC AAC CAG 1892
 Ile Thr Phe Ser Cys His Phe Tyr Asp Phe Phe Asn Gln
 470 475 480

GCT GAG TGG GAG CGT AGC TTC CGG GAC TAT GTG CTA TGC 1931
 Ala Glu Trp Glu Arg Ser Phe Arg Asp Tyr Val Leu Cys
 485 490

FIG. 1C

4 / 24

CAA	GCC	AAT	GTG	ACC	ATT	GGG	CTG	CCT	ACC	AAG	AAG	CCC	1970
Gln	Ala	Asn	Val	Thr	Ile	Gly	Leu	Pro	Thr	Lys	Lys	Pro	
495					500					505			
ATT	CCT	GAT	TGT	GAG	ATC	AAG	AAT	CGG	CCC	AGC	CTC	CTG	2009
Ile	Pro	Asp	Cys	Glu	Ile	Lys	Asn	Arg	Pro	Ser	Leu	Leu	
	510					515						520	
GTG	GAG	AAG	ATC	AAT	CTG	TTT	GCC	ATG	TTT	GGC	ACT	GGC	2048
Val	Glu	Lys	Ile	Asn	Leu	Phe	Ala	Met	Phe	Gly	Thr	Gly	
				525					530				
ATT	GCC	ATG	AGC	ACC	TGG	GTC	TGG	ACC	AAG	GCC	ACC	CTG	2087
Ile	Ala	Met	Ser	Thr	Trp	Val	Trp	Thr	Lys	Ala	Thr	Leu	
	535					540					545		
CTC	ATC	TGG	AGG	CGC	ACC	TGG	TGC	AGG	TTG	ACT	GGG	CAC	2126
Leu	Ile	Trp	Arg	Arg	Thr	Trp	Cys	Arg	Leu	Thr	Gly	His	
			550					555					
AGT	GAT	GAT	GAA	CCC	AAG	AGA	ATC	AAG	AAA	AGC	AAG	ATG	2165
Ser	Asp	Asp	Glu	Pro	Lys	Arg	Ile	Lys	Lys	Ser	Lys	Met	
560					565					570			
ATT	GCC	AAG	GCC	TTC	TCT	AAG	CGG	CGT	GAA	CTG	CTG	CAG	2204
Ile	Ala	Lys	Ala	Phe	Ser	Lys	Arg	Arg	Glu	Leu	Leu	Gln	
	575						580					585	
AAC	CCG	GGC	CAG	GAG	CTC	TCC	TTC	AGC	ATG	CAC	ACT	GTC	2243
Asn	Pro	Gly	Gln	Glu	Leu	Ser	Phe	Ser	Met	His	Thr	Val	
				590					595				
TCC	CAT	GAT	GGA	CCT	GTT	GCC	GGT	TTG	GCT	TTT	GAA	CTC	2282
Ser	His	Asp	Gly	Pro	Val	Ala	Gly	Leu	Ala	Phe	Glu	Leu	
	600					605					610		
AAT	GAA	CCC	TCA	GCT	GAT	GTC	TCC	TCT	GCC	TGG	GCC	CAG	2321
Asn	Glu	Pro	Ser	Ala	Asp	Val	Ser	Ser	Ala	Trp	Ala	Gln	
			615					620					
CAC	GTC	ACC	AAG	ATG	GTG	GCT	CGA	AGA	GGA	GCC	ATA	TTA	2360
His	Val	Thr	Lys	Met	Val	Ala	Arg	Arg	Gly	Ala	Ile	Leu	
	625				630					635			
CCC	CAG	GAT	GTG	TCT	GTC	ACC	CCT	GTG	GCA	ACT	CCA	GTG	2399
Pro	Gln	Asp	Val	Ser	Val	Thr	Pro	Val	Ala	Thr	Pro	Val	
	640						645					650	
CCA	CCA	GAA	GAA	CAA	GCC	AAC	CTG	TGG	CTG	GTT	GAG	GCA	2438
Pro	Pro	Glu	Glu	Gln	Ala	Asn	Leu	Trp	Leu	Val	Glu	Ala	
				655					660				

FIG. 1D

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5/24

GAG ATC TCC CCA GAG TTA GAG AAG CGT TTA GGC CGG AAG 2477
 Glu Ile Ser Pro Glu Leu Glu Lys Arg Leu Gly Arg Lys
 665 670 675

AAG AAG CGG AGG AAG AGG AAG AAG GAG GTG TGC CCC TTG 2516
 Lys Lys Arg Arg Lys Arg Lys Lys Glu Val Cys Pro Leu
 680 685

GGG CCA GCC CCT GAA CTT CAC CAC TCT GCC CCT GTT CCT 2555
 Gly Pro Ala Pro Glu Leu His His Ser Ala Pro Val Pro
 690 695 700

GCC ACC AGT GCA GTT CCT CGG CTG CCT CAG CTG CCT CGG 2594
 Ala Thr Ser Ala Val Pro Arg Leu Pro Gln Leu Pro Arg
 705 710 715

CAG AAG TGC CTA GTA GCT GCA AAT GCC TGG GGA ACA GGA 2633
 Gln Lys Cys Leu Val Ala Ala Asn Ala Trp Gly Thr Gly
 720 725

GAG CCC TGC CGA CAG GGA GCC TGG ACT GTA GTC TCC AAC 2672
 Glu Pro Cys Arg Gln Gly Ala Trp Thr Val Val Ser Asn
 730 735 740

CCC TTC TGC CCA GAG CCT AGT CCC CAT CAA GAT CCA TTT 2711
 Pro Phe Cys Pro Glu Pro Ser Pro His Gln Asp Pro Phe
 745 750

CTC CCT GGT GCC TCA GCC CCC AGG GTC TGG GCT CAG GGC 2750
 Leu Pro Gly Ala Ser Ala Pro Arg Val Trp Ala Gln Gly
 755 760 765

CGC CTC CAG GGG CTG GGA TCC ATT CAT TCC CGC ACT AAC 2789
 Arg Leu Gln Gly Leu Gly Ser Ile His Ser Arg Thr Asn
 770 775 780

CTA ATG GAG GCT GAG CTC TTG GAT GCA GAC TCG GAC TTC TG 2830
 Leu Met Glu Ala Glu Leu Leu Asp Ala Asp Ser Asp Phe
 785 790 793

AGCTTGCAGG GCAGGTCCTA GGATGGGGAA GACAAGTGCA CGCCTTCCTA 2880
 TAGCTCTTCC TGAGAGCACA CCTCTGGGGT CTCATCTGAC AGTCTATGGG 2930
 CCATGTATCT GCCTACAAGA GCTGTGTACG ACTGGCTAGA AGCAGCCAGA 2980
 CCATAGAAAC AAGCTGAACA CAGCCACTGA TAGACCTCAC TTCAGAAGCA 3030
 AGACCTGCAG TTCAGGACCC TTGCCTCTGC CCCCCAATTA GAGTCTGGCT 3080
 GGCAGTGTTA GTCTCCAACA GAGCTTGTAC TAGGGTAGGA ACGGCAGAGG 3130
 CAGGGGTGAT GGTACCCAGA GTGGGCTGGG GTGTCCAGTG AGGTAACCAA 3180

FIG. 1E

SUBSTITUTE SHEET (RULE 26)

6/24

GCCCATGTCT GGCAGATGAG GGCTGGCTGC CCTTTTCTGT GCCAATGAGT 3230
GCCCTTTTCT GGCCTCTGA GACCAAAAGT GTTTATTGTG TCATTTGTCC 3280
TTTTTCTAGG TGGGAACAGG ACTCTCTTTT TCCTCTTCCT GGTAGTTGTA 3330
ATGACTACTC CCATAAGGCC TAGAACTGCT CTCAGTAGGT GGCCCTGTCC 3380
AAAACACATC TTCACATCTT AGTTCCACTA GGCCAAACTC TTATTGGTTA 3430
GCACCTTAAA ACACACACAC ACACACACAC ACACACACAC ACACACACAC 3480
ACACACACAC ACCCTCTTAC TTCTGAGCTT GGTCTCAAGA GAGAGACAAC 3530
TGGTTCAGCT CCAGGCCTCT GAGAGTCATG TTTTCTTCCT CACATCCATC 3580
CAGTGGGGAT GGATCCTCTG ACTTAAGGGG CTACCTTGGG AAGCCTCTGT 3630
AGCTTCAGCC AGGCAAGAAA GCTTCTTCCA ACTTCTGTAT CTGGTGGGAA 3680
GGAGGACTCC CTACTTTTTA CAATGTCTAG TCATTTTCAT AGTGCCCCAC 3730
ATTCAAGAAC CAGACAGCAG GATGCCTTAG AAGCTGGCTG GGTTCAGGT 3780
CAGAGGCTCA GTATGAGAAG AAGAAATATG AACAGTAAAT AAAACATTTT 3830
TGTATAAAAA AAAAAAAAAA AAAA 3854

FIG. 1F

rSmo	1	M A A G R P V R G P E L A P R R L L Q L L . L L V L L G G R G R G A A L S G N V T G P G P R S A G G
dSmo	1	M Q Y L N F P R M P N I M M F L E V A I L C L W V V A D A S A S S A K F G S T T P A S A Q Q S D V E
rSmo	50	S A R R N A P V T S P P P P L L S H C G R A A H C E P L R Y . . N V C
dSmo	51	L E P I N G T L N Y R L Y A K X G R D D K P W F D G L D S R H I Q C V R R A R C Y P T S N A T N T C
rSmo	83	L G S A L P Y G A T T L L A G D S D S Q E E A H S K L V L W S G L R N A P R C W A V I Q P L L C A
dSmo	101	F G S K L P Y E L S S L D L T . D F H T E K E L N D K L N D Y Y A L K H V P K C W A A I Q P F L C A
rSmo	133	V Y M P K C E N D R V E L P S R T L C Q A T R G P C A I V E R E R G W P D F L R C T P D H F
dSmo	150	V F K P K C E K I N G E D M V Y L P S Y E M C R I T M E P C R I L Y N T T F P K F L R C N E T L E
rSmo	179	P E G C P N E V Q N I K F N S S G Q C C E A P L V R T D N P K S W Y E D V E G C G I Q C Q N P L F T E
dSmo	200	P T K C T N G A R G M K F N G T G Q C L S P L V P T D T S A S Y Y P G I E G C G V R C K D P L Y T D
rSmo	229	A E H Q D M H S Y I A A P Q A W T G L C V L F T L A T F V A D W R N S N R Y P A V I L F Y V N A C F F
dSmo	250	D E H R Q I H K L I G W A G S I C L L S N L F V V S T F F I D W K N A N K Y P A V I V F Y I N L C F F
rSmo	279	F V G S I G W L A Q F M D G A R R E I V C R A D G T M R F G E P T S S E T L S C V I I F V I V Y Y A
dSmo	300	L I A C V G W L L Q F T S G S R E D I V C R K D G T L R H S E P T A G E N L S C I V I F V L V Y Y F
rSmo	329	L M A G V V W F V V L T Y A W H T S F K A L G T T Y Q P L S G K T S Y F H L L T W S L P F V L T V A
dSmo	350	L T A G M V W F V F L T Y A W H . . W R A M G H V Q D R I D K K G S Y F H L V A W S L P L V L T I T
rSmo	379	I L A V A Q V D G D S V S G I C F V G Y K N Y R Y R A G F V L A P I G L V L T V G G Y F Q I R G V M
dSmo	398	T M A F S E V D G N S I V G I C F V G Y I N H S M R A G L L G P L C G V I L L G G Y F I T R G M V
rSmo	429	T L F S I K S N H P G L L S E K A A S K I N E T M L R L G T F G F L A F G F V L I T F S C H F Y D F
dSmo	448	M L F G L K H F A N D I K S T S A S N K I H L I I M R M G V C A L L T L V F I L V A I A C H V T E F

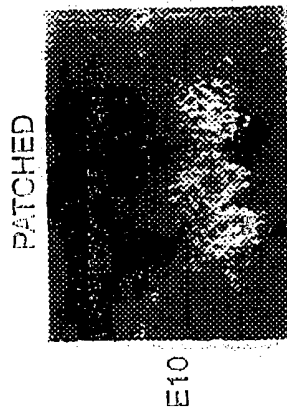
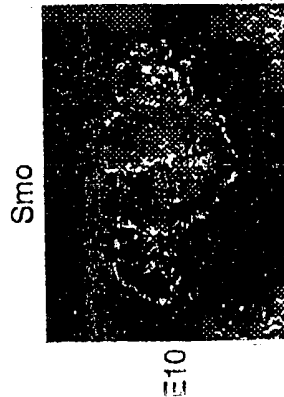
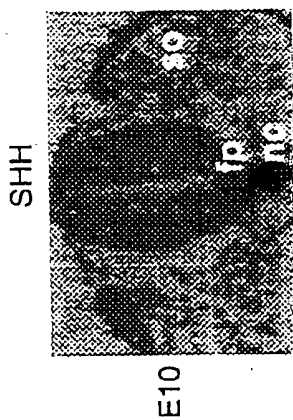
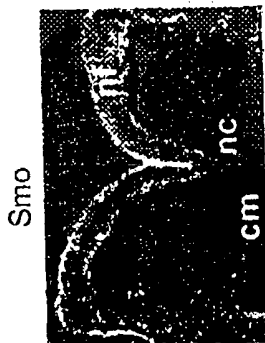
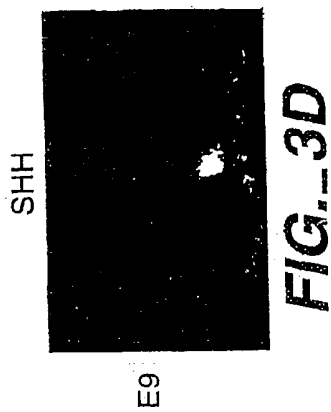
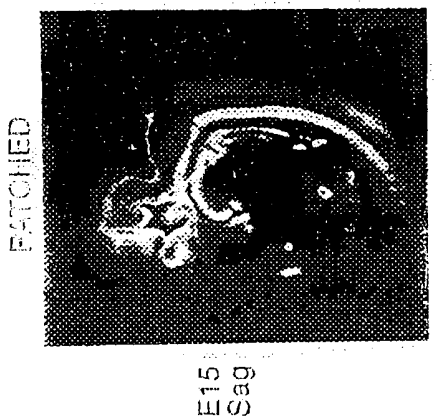
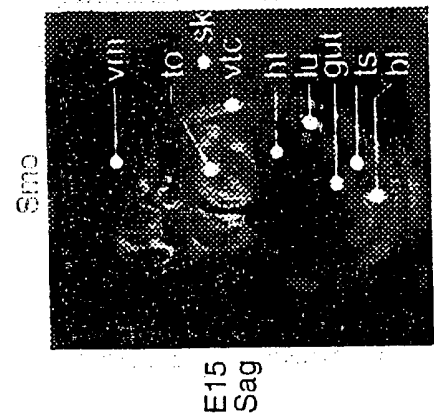
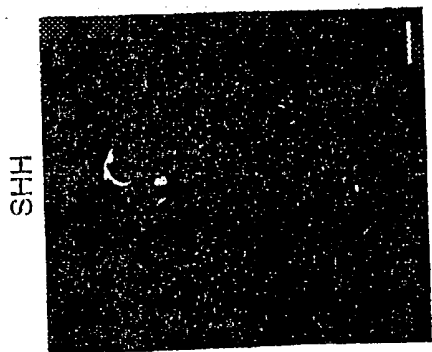
FIG. 2A

8/24

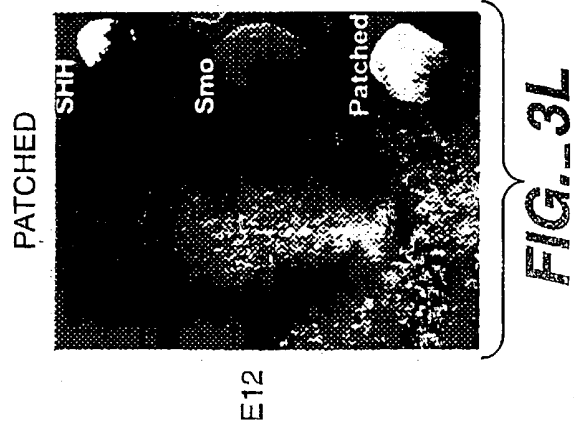
rSmo	479	F N Q A E W E R S F R D Y V L C Q A N Y T I G L P T K K P I P D C E I K N R P S L L V E K I N L F A
dSmo	498	R H A D E W A Q S F R Q F I I C . . K I S S V F E E K . . S S C R I E N R P S V G V L Q L H L L C
rSmo	529	M F G T G I A M S T W V W T K A T L L I W R R T W C R L T G H S D D E P K R I K K S K M I A K A F S
dSmo	543	L F S S G I V M S T W C W T P S S I E T W K R Y I R K K C G K E V V E V K M P K H K V I A Q T W A
rSmo	579	K R R E L L Q N P G Q E L S F S M H T V S H D G P V A G L A F E L N E . . . P S A D V S S A W A Q
dSmo	593	K R K D . F E D K G R . L S I T L Y N . T H T D P V . G L N F D V N D L N S S E T N D I S S T W A A
rSmo	625	H V T K M V A R R . . . G A I L P Q D V S V T P V A T P V P P E E Q A N L W L V E
dSmo	639	Y L P Q C V K R R M A L T G A A T G N S S S H G P R K N S L D S E I S V S V R H V S V E S R R N S V
rSmo	663	A E I S P E L E K R L G R K K K R R K R K K E V C P L G P A P E L H H S A P V P A T S A V P R L P Q
dSmo	689	D S Q V S V K I A E M K T K V A S R S R G K H G G S S S N R R T Q R R R D Y I A A A T . . G K S S R
rSmo	713	L P R Q K C L V A A N A W G T G E P C R Q G A W T V V S N P F C P E P S P H Q D P F L P G A S A P R
dSmo	737	R R E S S T S V E S Q V I A L K K T T Y P N A S H K V G V F A H S S K K Q H N Y T S S M K R R T A
rSmo	763	V W A Q G R L Q G L G S I H S R T N L M E A E L L D A D S D F
dSmo	787	N A G L D P S I L N E F L Q K N G D F I F P F L Q N Q D M S S S S E E D N S R A S Q K I Q D L N V V
dSmo	837	V K Q Q E I S E D D H D G I K I E E L P N S K Q V A L E N F L K N I K K S N E S N S N R H S R N S A
dSmo	887	R S Q S K K S Q K R H L K N P A A D L D F R K D C V K Y R S N D S L S C S S E E L D V A L D V G S L
dSmo	937	L N S S F S G I S M G K P H S R N S K T S C D V G I Q A N P F E L V P S Y G E D E L Q Q A M R L L N
dSmo	987	A A S R Q R T E A A N E D F G G T E L Q G L L G H S H R H Q R E P T F M S E S D K L K M L L L P S K

FIG. 2B

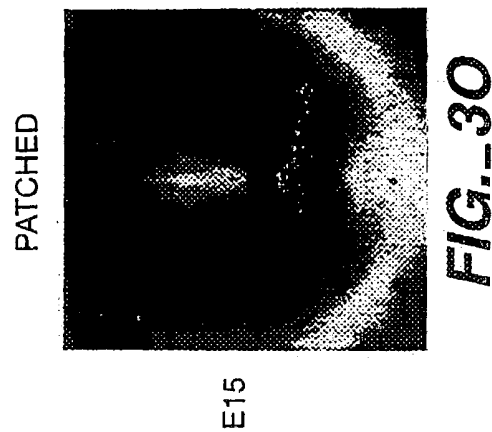
9 / 24



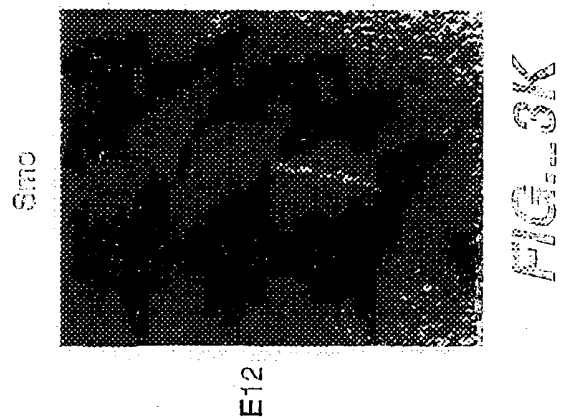
10 / 24



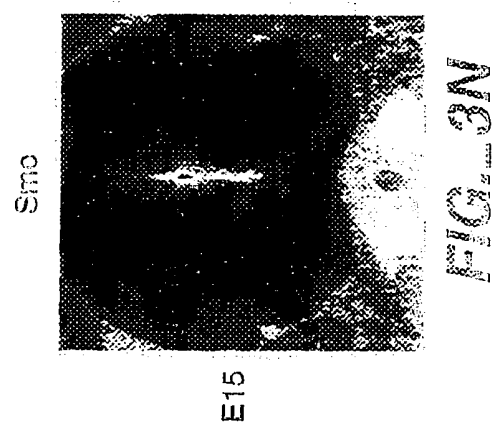
E12



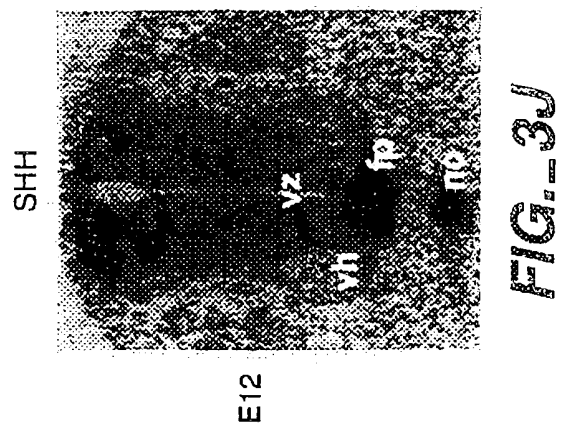
E15



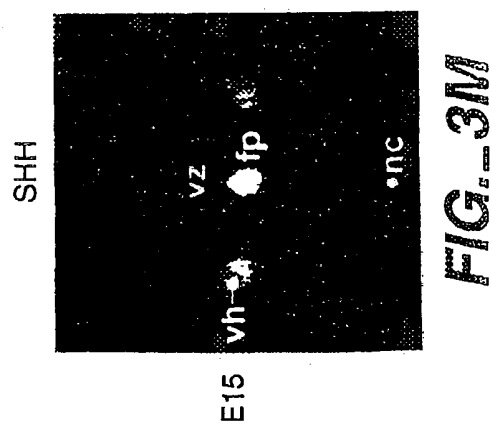
E12



E15



E12



E15

11 / 24

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1  CGGGGGTTGG CCATGGCCGC TGCCCGCCCA GCGCGGGGGC CGGAGCTCCC
   GCCCCAACC GGTACCGGCG ACGGGCGGGT CGCGCCCCCG GCCTCGAGGG
1  MetAlaAl aAlaArgPro AlaArgGlyP roGluLeuPr
   Met
51  GCTCCTGGGG CTGCTGCTGC TGCTGCTGCT GGGGGACCCG GGCCGGGGGG
   CGAGGACCCC GACGACGACG ACGACGACGA CCCCCTGGGC CCGGCCCCCC
14  oLeuLeuGly LeuLeuLeuL euLeuLeuLe uGlyAspPro GlyArgGlyAla
101 CGGCCTCGAG CGGGAACGCG ACCGGGCCTG GGCCTCGGAG CGCGGGCGGG
   GCCGGAGCTC GCCCTTGCGC TGGCCCGGAC CCGGAGCCTC GCGCCCCGCC
31  AlaSerSe rGlyAsnAla ThrGlyProG lyProArgSe rAlaGlyGly
151 AGCGCGAGGA GGAGCGCGGC GGTGACTGGC CCTCCGCCGC CGCTGAGCCA
   TCGCGCTCCT CCTCGCGCCG CCACTGACCG GGAGGCGGGC GCGACTCGGT
47  SerAlaArgA rgSerAlaAl aValThrGly ProProProP roLeuSerHis
201 CTGCGGCCGG GCTGCCCCCT GCGAGCCGCT GCGCTACAAC GTGTGCCTGG
   GACGCCGGCC CGACGGGGGA CGCTCGGCGA CGCGATGTTG CACACGGACC
64  CysGlyArg AlaAlaProC ysGluProLe uArgTyrAsn ValCysLeuG
251 GCTCGGTGCT GCCCTACGGG GCCACCTCCA CACTGCTGGC CGGAGACTCG
   CGAGCCACGA CGGGATGCCC CGGTGGAGGT GTGACGACCG GCCTCTGAGC
81  lySerValLe uProTyrGly AlaThrSerT hrLeuLeuAl aGlyAspSer
301 GACTCCCAGG AGGAAGCGCA CGGCAAGCTC GTGCTCTGGT CGGGCCTCCG
   CTGAGGGTCC TCCTTCGCGT GCCGTTTCGAG CACGAGACCA GCCCGGAGGC
97  AspSerGlnG luGluAlaHi sGlyLysLeu ValLeuTrpS erGlyLeuAr
351 GAATGCCCCC CGCTGCTGGG CAGTGATCCA GCCCCTGCTG TGTGCCGTAT
   CTTACGGGGG GCGACGACCC GTCACTAGGT CGGGGACGAC ACACGGCATA
114 gAsnAlaPro ArgCysTrpA laValIleGl nProLeuLeu CysAlaValTyr
401 ACATGCCCAA GTGTGAGAAT GACCGGGTGG AGCTGCCCAG CCGTACCCTC
   TGTACGGGTT CACACTCTTA CTGGCCCACC TCGACGGGTC GGCATGGGAG
131 MetProLy sCysGluAsn AspArgValG luLeuProSe rArgThrLeu
451 TGCCAGGCCA CCCGAGGCC CTGTGCCATC GTGGAGAGGG AGCGGGGCTG
   ACGGTCCGGT GGGCTCCGGG GACACGGTAG CACCTCTCCC TCGCCCCGAC
147 CysGlnAlaT hrArgGlyPr oCysAlaIle ValGluArgG luArgGlyTrp
501 GCCTGACTTC CTGCGCTGCA CTCCTGACCG CTTCCCTGAA GGCTGCACGA
   CGGACTGAAG GACGCGACGT GAGGACTGGC GAAGGGACTT CCGACGTGCT
164 ProAspPhe LeuArgCysT hrProAspAr gPheProGlu GlyCysThra
551 ATGAGGTGCA GAACATCAAG TTCAACAGTT CAGGCCAGTG CGAAGTGCCC
   TACTCCACGT CTTGTAGTTC AAGTTGTCAA GTCCGGTCAC GCTTCACGGG
181 snGluValGl nAsnIleLys PheAsnSerS erGlyGlnCy sGluValPro
601 TTGGTTTCGA CAGACAACCC CAAGAGCTGG TACGAGGACG TGGAGGGCTG
   AACCAAGCCT GTCTGTTGGG GTTCTCGACC ATGCTCCTGC ACCTCCCGAC
197 LeuValArgT hrAspAsnPr oLysSerTrp TyrGluAspV alGluGlyCy

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FIG. 4A

SUBSTITUTE SHEET (RULE 26)

12/24

651 CGGCATCCAG TGCCAGAACC CGCTCTTCAC AGAGGCTGAG CACCAGGACA
 GCCGTAGGTC ACGGTCTTGG GCGAGAAGTG TCTCCGACTC GTGGTCCTGT
 214 sGlyIleGln CysGlnAsnP roLeuPheTh rGluAlaGlu HisGlnAspMet
 701 TGCACAGCTA CATCGCGGCC TTCGGGGCCG TCACGGGCCT CTGCACGCTC
 ACGTGTTCGAT GTAGCGCCGG AAGCCCCGGC AGTGCCCGGA GACGTGCGAG
 231 HisSerTy rIleAlaAla PheGlyAlaV alThrGlyLe uCysThrLeu
 751 TTCACCCTGG CCACATTCGT GGCTGACTGG CGGAACCTCGA ATCGCTACCC
 AAGTGGGACC GGTGTAAGCA CCGACTGACC GCCTTGAGCT TAGCGATGGG
 247 PheThrLeuA laThrPheVa lAlaAspTrp ArgAsnSera snArgTyrPro
 801 TGCTGTATT CTCTTCTACG TCAATGCGTG CTTCTTTGTG GGCAGCATTG
 ACCACAATAA GAGAAGATGC AGTTACGCAC GAAGAAACAC CCGTCGTAAC
 264 AlaValIle LeuPheTyrV alAsnAlaCy sPhePheVal GlySerIleG
 start clone 14
 851 GCTGGCTGGC CCAGTTCATG GATGGTGCCC GCCGAGAGAT CGTCTGCCGT
 CGACCGACCG GGTCAAGTAC CTACCACGGG CGGCTCTCTA GCAGACGGCA
 281 lyTrpLeuAl aGlnPheMet AspGlyAlaA rgArgGluIl eValCysArg
 901 GCAGATGGCA CCATGAGGCT TGGGGAGCCC ACCTCCAATG AGACTCTGTC
 CGTCTACCGT GGTACTCCGA ACCCCTCGGG TGGAGGTTAC TCTGAGACAG
 297 AlaAspGlyT hrMetArgLe uGlyGluPro ThrSerAsnG luThrLeuSe
 951 CTGCGTCATC ATCTTTGTCA TCGTGTACTA CGCCCTGATG GCTGGTGTGG
 GACGCAGTAG TAGAAACAGT AGCACATGAT GCGGGACTAC CGACCACACC
 314 rCysValIle IlePheValI leValTyrTy rAlaLeuMet AlaGlyValVal
 1001 TTTGGTTTGT GGTCCCTCACC TATGCCTGGC ACACTTCCTT CAAAGCCCTG
 AAACCAAACA CCAGGAGTGG ATACGGACCG TGTGAAGGAA GTTTCGGGAC
 331 TrpPheVa lValLeuThr TyrAlaTrpH isThrSerPh eLysAlaLeu
 1051 GGCACCACCT ACCAGCCTCT CTCGGGCAAG ACCTCCTACT TCCACCTGCT
 CCGTGGTGGG TGGTCGGAGA GAGCCCGTTC TGGAGGATGA AGGTGGACGA
 347 GlyThrThrT yrGlnProLe uSerGlyLys ThrSerTyrP heHisLeuLeu
 1101 CACCTGGTCA CTCCCCTTTG TCCTCACTGT GGCAATCCTT GCTGTGGCGC
 GTGGACCACT GAGGGGAAAC AGGAGTGACA CCGTTAGGAA CGACACCGCG
 364 ThrTrpSer LeuProPheV alLeuThrVa lAlaIleLeu AlaValAlaG
 1151 AGGTGGATGG GGA CTCTGTG AGTGGCATTG GTTTTGTGGG CTACAAGAAC
 TCCACCTACC CCTGAGACAC TCACCGTAAA CAAAACACCC GATGTTCTTG
 381 lnValAspGl yAspSerVal SerGlyIleC ysPheValGl yTyrLysAsn
 1201 TACCGATACC GTGCGGGCTT CGTGCTGGCC CCAATCGGCC TGGTGCTCAT
 ATGGCTATGG CACGCCCGAA GCACGACCGG GGTAGCCGG ACCACGAGTA
 397 TyrArgTyrA rgAlaGlyPh eValLeuAla ProIleGlyL euValLeuIl
 1251 CGTGGGAGGC TACTTCCTCA TCCGAGGAGT CATGACTCTG TTCTCCATCA
 GCACCCTCCG ATGAAGGAGT AGGCTCCTCA GTACTGAGAC AAGAGGTAGT
 414 eValGlyGly TyrPheLeuI leArgGlyVa lMetThrLeu PheSerIleLys

FIG. 4B

SUBSTITUTE SHEET (RULE 26)

13 / 24

1301	AGAGCAACCA	CCCCGGGCTG	CTGAGTGAGA	AGGCTGCCAG	CAAGATCAAC
	TCTCGTTGGT	GGGGCCCGAC	GACTCACTCT	TCCGACGGTC	GTTCTAGTTG
431	SerAsnHi	sProGlyLeu	LeuSerGluL	ysAlaAlaSe	rLysIleAsn
1351	GAGACCATGC	TGCGCCTGGG	CATTTTGGC	TTCTGGCCT	TTGGCTTTGT
	CTCTGGTACG	ACGCGGACCC	GTA AAAACCG	AAGGACCGGA	AACCGAAACA
447	GluThrMetL	euArgLeuGl	yIlePheGly	PheLeuAlaP	heGlyPheVal
1401	GCTCATTACC	TTCAGCTGCC	ACTTCTACGA	CTTCTTCAAC	CAGGCTGAGT
	CGAGTAATGG	AAGTCGACGG	TGAAGATGCT	GAAGAAGTTG	GTCCGACTCA
464	LeuIleThr	PheSerCysH	isPheTyrAs	pPhePheAsn	GlnAlaGluT
1451	GGGAGCGCAG	CTTCCGGGAC	TATGTGCTAT	GTCAGGCCAA	TGTGACCATC
	CCCTCGCGTC	GAAGGCCCTG	ATACACGATA	CAGTCCGGTT	ACACTGGTAG
481	rpGluArgSe	rPheArgAsp	TyrValLeuC	ysGlnAlaAs	nValThrIle
1501	GGGCTGCCCA	CCAAGCAGCC	CATCCCTGAC	TGTGAGATCA	AGAATCGCCC
	CCCGACGGGT	GGTTCGTCGG	GTAGGGACTG	ACACTCTAGT	TCTTAGCGGG
497	GlyLeuProT	hrLysGlnPr	oIleProAsp	CysGluIleL	ysAsnArgPr
1551	GAGCCTTCTG	GTGGAGAAGA	TCAACCTGTT	TGCCATGTTT	GGAAC TGGCA
	CTCGGAAGAC	CACCTCTTCT	AGTTGGACAA	ACGGTACAAA	CCTTGACCGT
514	oSerLeuLeu	ValGluLysI	leAsnLeuPh	eAlaMetPhe	GlyThrGlyIle
1601	TCGCCATGAG	CACCTGGGTC	TGGACCAAGG	CCACGCTGCT	CATCTGGAGG
	AGCGGTACTC	GTGGACCCAG	ACCTGGTTCC	GGTGCGACGA	G TAGACCTCC
531	AlaMetSe	rThrTrpVal	TrpThrLysA	laThrLeuLe	uIleTrpArg
1651	CGTACCTGGT	GCAGGTTGAC	TGGGCAGAGT	GACGATGAGC	CAAAGCGGAT
	GCATGGACCA	CGTCCA ACTG	ACCCGTCTCA	CTGCTACTCG	GTTTCGCCTA
547	ArgThrTrpC	ysArgLeuTh	rGlyGlnSer	AspAspGluP	roLysArgIle
1701	CAAGAAGAGC	AAGATGATTG	CCAAGGCCTT	CTCTAAGCGG	CACGAGCTCC
	GTTCTTCTCG	TTCTACTAAC	GGTTCCGGAA	GAGATTGCGC	GTGCTCGAGG
564	LysLysSer	LysMetIleA	laLysAlaPh	eSerLysArg	HisGluLeuL
1751	TGCAGAACCC	AGGCCAGGAG	CTGTCCTTCA	GCATGCACAC	TGTGTCCCAC
	ACGTCTTGGG	TCCGGTCCTC	GACAGGAAGT	CGTACGTGTG	ACACAGGGTG
581	euGlnAsnPr	oGlyGlnGlu	LeuSerPheS	erMetHisTh	rValSerHis
1801	GACGGGCCCC	TGGCGGGCTT	GGCCTTTGAC	CTCAATGAGC	CCTCAGCTGA
	CTGCCCCGGC	ACCGCCCGAA	CCGGAAACTG	GAGTTACTCG	GGAGTCGACT
597	AspGlyProV	alAlaGlyLe	uAlaPheAsp	LeuAsnGluP	roSerAlaAs
1851	TGTCTCCTCT	GCCTGGGCCC	AGCATGTCAC	CAAGATGGTG	GCTCGGAGAG
	ACAGAGGAGA	CGGACCCGGG	TCGTACAGTG	GTTCTACCAC	CGAGCCTCTC
614	pValSerSer	AlaTrpAlaG	lnHisValTh	rLysMetVal	AlaArgArgGly
			end clone 5		
1901	GAGCCATACT	GCCCCAGGAT	ATTTCTGTCA	CCCCTGTGGC	AACTCCAGTG
	CTCGGTATGA	CGGGGTCCTA	TAAAGACAGT	GGGGACACCG	TTGAGGTCAC
631	AlaIleLe	uProGlnAsp	IleSerValT	hrProValAl	aThrProVal

FIG. 4C

SUBSTITUTE SHEET (RULE 26)

14 / 24

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1951  CCCCCAGAGG  AACAAGCCAA  CCTGTGGCTG  GTTGAGGCAG  AGATCTCCCC
      GGGGGTCTCC  TTGTTTCGGTT  GGACACCGAC  CAACTCCGTC  TCTAGAGGGG
647   ProProGluG  luGlnAlaAs  nLeuTrpLeu  ValGluAlaG  luIleSerPro

2001  AGAGCTGCAG  AAGCGCCTGG  GCCGGAAGAA  GAAGAGGAGG  AAGAGGAAGA
      TCTCGACGTC  TTCGCGGACC  CGGCCTTCTT  CTTCTCCTCC  TTCTCCTTCT
664   GluLeuGln  LysArgLeuG  lyArgLysLy  sLysArgArg  LysArgLysL

2051  AGGAGGTGTG  CCCGCTGGCG  CCGCCCCCTG  AGCTTCACCC  CCCTGCCCCT
      TCCTCCACAC  GGGCGACCGC  GGCGGGGGAC  TCGAAGTGGG  GGGACGGGGA
681   ysGluValCy  sProLeuAla  ProProProG  luLeuHisPr  oProAlaPro

2101  GCCCCAGTA  CCATTCTCTG  ACTGCCTCAG  CTGCCCCGGC  AGAAATGCCT
      CGGGGGTCAT  GGTAAGGAGC  TGACGGAGTC  GACGGGGCCG  TCTTTACGGA
697   AlaProSerT  hrIleProAr  gLeuProGln  LeuProArgG  lnLysCysLe

2151  GGTGGCTGCA  GGTGCCTGGG  GAGCTGGGGA  CTCTTGCCGA  CAGGGAGCGT
      CCACCGACGT  CCACGGACCC  CTCGACCCCT  GAGAACGGCT  GTCCCTCGCA
714   uValAlaAla  GlyAlaTrpG  lyAlaGlyAs  pSerCysArg  GlnGlyAlaTrp

2201  GGACCCTGGT  CTCCAACCCA  TTCTGCCCAG  AGCCCAGTCC  CCCTCAGGAT
      CCTGGGACCA  GAGGTGGGGT  AAGACGGGTC  TCGGGTCAGG  GGGAGTCCTA
731   ThrLeuVa  lSerAsnPro  PheCysProG  luProSerPr  oProGlnAsp

2251  CCATTTCTGC  CCAGTGCACC  GGCCCCCGTG  GCATGGGCTC  ATGGCCGCCG
      GGTAAAGACG  GGTCACGTGG  CCGGGGGCAC  CGTACCCGAG  TACCGGCGGC
747   ProPheLeuP  roSerAlaPr  oAlaProVal  AlaTrpAlaH  isGlyArgArg

2301  ACAGGGCCTG  GGGCCTATTC  ACTCCCGCAC  CAACCTGATG  GACACAGAAC
      TGTCCCGGAC  CCCGGATAAG  TGAGGGCGTG  GTTGGACTAC  CTGTGTCTTG
764   GlnGlyLeu  GlyProIleH  isSerArgTh  rAsnLeuMet  AspThrGluL

2351  TCATGGATGC  AGACTCGGAC  TTCTGAGCCT  GCAGAGCAGG  ACCTGGGACA
      AGTACCTACG  TCTGAGCCTG  AAGACTCGGA  CGTCTCGTCC  TGGACCCTGT
781   euMetAspAl  aAspSerAsp  Phe
      Stop

2401  GGAAAGAGAG  GAACCAATAC  CTTCAAGGCT  CTTCTTCCTC  ACCGAGCATG
      CCTTTCTCTC  CTTGGTTATG  GAAGTTCCGA  GAAGAAGGAG  TGGCTCGTAC

2451  CTTCCCTAGG  ATCCCGTCTT  CCAGAGAACC  TGTGGGCTGA  CTGCCCTCCG
      GAAGGGATCC  TAGGGCAGAA  GGTCTCTTGG  ACACCCGACT  GACGGGAGGC

2501  AAGAGAGTTC  TGGATGTCTG  GCTCAAAGCA  GCAGGACTGT  GGGAAAGAGC
      TTCTCTCAAG  ACCTACAGAC  CGAGTTTCGT  CGTCCTGACA  CCCTTTCTCG

2551  CTAACATCTC  CATGGGGAGG  CCTCACCCCA  GGGACAGGGC  CCTGGAGCTC
      GATTGTAGAG  GTACCCCTCC  GGAGTGGGGT  CCCTGTCCCG  GGACCTCGAG

2601  AGGGTCCTTG  TTTCTGCCCT  GCCAGCTGCA  GCCTGGTTGG  CAGCATCTGC
      TCCAGGAAC  AAAGACGGGA  CGGTGACGTC  CGGACCAACC  GTCGTAGACG

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FIG. 4D

15 / 24

2651 TCCATCGGGG CAGGGGGTAT GCAGAGCTTG TGGTGGGGCA GGAACGGTGG
AGGTAGCCCC GTCCCCCATA CGTCTCGAAC ACCACCCCGT CCTTGCCACC

2701 AGGCAGAGGT GACAGTTCCC AGAGTGGGCT TTGGTGGCCA GGGAGGCAGC
TCCGTCTCCA CTGTCAAGGG TCTCACCCGA AACCACCGGT CCCTCCGTCG

2751 CTAGCCTATG TCTGGCAGAT GAGGGCTGGC TGCCGTTTTT TGGGCTGATG
GATCGGATAC AGACCGTCTA CTCCCGACCG ACGGCAAAG ACCCGACTAC

2801 GGTGCCCTTT CCTGGCAGTC TCAGTCCAAA AGTGTTGACT GTGTCATTAG
CCACGGGAAA GGACCGTCAG AGTCAGGTTT TCACAACTGA CACAGTAATC

2851 TCCTTTGTCT AAGTAGGGCC AGGGCACCGT ATTCCTCTCC CAGGTGTTTG
AGGAAACAGA TTCATCCCGG TCCCGTGGCA TAAGGAGAGG GTCCACAAAC

2901 TGGGGCTGGA AGGACCTGCT CCCACAGGGG CCATGTCCTC TCTTAATAGG
ACCCCGACCT TCCTGGACGA GGGTGTCCCC GGTACAGGAG AGAATTATCC

2951 TGGCACTACC CCAAACCCAC CG
ACCGTGATGG GGTTTGGGTG GC

FIG._4E

hSno	1	MAAARPARGPE	LP	LLGLLLLLLLG
rat.sno	1	MAAGRPVRGPE	LAPRRLLQLLLVLG	
dros.sno	1	MHXRTAEQETGIQPIKIHTRQLFNDFYKRMQYLNFP	RMPNIMMFL	EVAIL
hSno	25	DPRGAASSGNATGPGPRSAGGSARRSAAVTGP		PP
rat.sno	28	GRGGAALSGNVVTGPGPRSAGGSARRNAPVTSP		PP
dros.sno	51	CLWVVDASSAKFGSTTPASAQQSDVELEPINGTLNYRLYAKKGRDDK		
hSno	60	PLS	HCGRAAPCEPLRY	NVCLGSVLPYGATSTLLAGDSDSQ
rat.sno	63	PLLS	HCGRAAHCEPLRY	NVCLGSALPYGATTLLAGDSDSQ
dros.sno	101	PWFDGLDSRHIQCVRRAARCYPTSNATNTCFGSKLPYELSLDLT		DFHTE
hSno	100	EEAHGKLVLSGRLRNAPRCWAVIQPLLCAVYMPKCE		NDRVELPSRT
rat.sno	104	EEAHSKLVLSGRLRNAPRCWAVIQPLLCAVYMPKCE		NDRVELPSRT
dros.sno	150	KELNDKLVNDYYALKHVPKCWAALQPFLLCAVFKPKCEKINGEDM		VYLPSE
hSno	146	LQATRGPCAIVERERGWPDFLRCCTPDR		FPEGCTNEVQNIKFNSSGQCEV
rat.sno	150	LQATRGPCAIVERERGWPDFLRCCTPDH		FPEGCPNEVQNIKFNSSGQCEA
dros.sno	200	MCRITMEPCRILYNTTFFPKFLRCNETLFP		TKCTNGARGMKFNGTGQCL

FIG. 5A

17/24

hSm	196	P	L	V	R	T	D	N	P	K	S	W	Y	E	D	V	E	G	C	G	I	Q	C	N	P	L	F	T	E	A	E	H	Q	D	M	H	S	Y	I	A	A	F	G	A	V	T	G	L	C	T	
rat. sm	200	P	L	V	R	T	D	N	P	K	S	W	Y	E	D	V	E	G	C	G	I	Q	C	N	P	L	F	T	E	A	E	H	Q	D	M	H	S	Y	I	A	A	F	G	A	V	T	G	L	C	T	
dros. sm	250	P	L	V	P	T	D	T	S	A	S	Y	P	G	I	E	G	C	G	V	R	C	K	D	P	L	Y	T	D	D	E	H	R	Q	I	H	K	L	I	G	W	A	G	S	I	C	L	L	S	N	
hSm	246	L	F	T	L	A	T	F	V	A	D	W	R	N	S	N	R	Y	P	A	V	I	L	F	Y	V	N	A	C	F	F	V	G	S	I	G	W	L	A	Q	F	M	D	G	A	R	R	E	I	V	C
rat. sm	250	L	F	T	L	A	T	F	V	A	D	W	R	N	S	N	R	Y	P	A	V	I	L	F	Y	V	N	A	C	F	F	V	G	S	I	G	W	L	A	Q	F	M	D	G	A	R	R	E	I	V	C
dros. sm	300	L	F	V	V	S	T	F	I	D	W	K	N	A	N	K	Y	P	A	V	I	V	F	Y	I	N	L	C	F	L	I	A	C	V	G	W	L	L	Q	F	T	S	G	S	R	E	D	I	V	C	
hSm	296	R	A	D	G	T	M	R	L	G	E	P	T	S	N	E	T	L	S	C	V	I	F	V	I	V	Y	Y	A	L	M	A	G	V	V	W	F	V	V	L	T	Y	A	W	H	T	S	F	K	A	
rat. sm	300	R	A	D	G	T	M	R	F	G	E	P	T	S	S	E	T	L	S	C	V	I	F	V	I	V	Y	Y	A	L	M	A	G	V	V	W	F	V	V	L	T	Y	A	W	H	T	S	F	K	A	
dros. sm	350	R	K	D	G	T	L	R	H	S	E	P	T	A	G	E	N	L	S	C	I	V	I	F	V	L	V	Y	Y	F	L	T	A	G	M	V	W	F	V	F	L	T	Y	A	W	H	-	W	R	A	
hSm	346	L	G	T	T	Y	Q	P	L	S	G	K	T	S	Y	F	H	L	L	T	W	S	L	P	F	V	L	T	V	A	I	L	A	V	A	Q	V	D	G	D	S	V	S	G	I	C	F	V	G	Y	K
rat. sm	350	L	G	T	T	Y	Q	P	L	S	G	K	T	S	Y	F	H	L	L	T	W	S	L	P	F	V	L	T	V	A	I	L	A	V	A	Q	V	D	G	D	S	V	S	G	I	C	F	V	G	Y	K
dros. sm	398	M	G	H	V	Q	D	R	I	D	K	K	G	S	Y	F	H	L	V	A	W	S	L	P	L	V	L	T	I	T	T	M	A	F	S	E	V	D	G	N	S	I	V	G	I	C	F	V	G	Y	I
hSm	396	N	Y	R	Y	R	A	G	F	V	L	A	P	I	G	L	V	L	I	V	G	G	Y	F	L	I	R	G	V	M	T	L	F	S	I	K	S	N	H	P	G	L	L	S	E	K	A	A	S	K	I
rat. sm	400	N	Y	R	Y	R	A	G	F	V	L	A	P	I	G	L	V	L	I	V	G	G	Y	F	L	I	R	G	V	M	T	L	F	S	I	K	S	N	H	P	G	L	L	S	E	K	A	A	S	K	I
dros. sm	448	N	H	S	M	R	A	G	L	L	L	G	P	L	C	G	V	I	L	I	G	G	Y	F	I	T	R	G	M	V	M	L	F	G	L	K	H	F	A	N	D	I	K	S	T	S	A	S	N	K	I

FIG. 5B

18/24

hSmO	446	NETMLRLGIFGFLAFGFVLITFSCHFYDFFNQAEWERSFRDYVLCQANVT
rat.smo	450	NETMLRLGIFGFLAFGFVLITFSCHFYDFFNQAEWERSFRDYVLCQANVT
dros.smo	498	HLIIMRMGVCALLTLVFILLVAIACHVTEFRHADEWAQSFQFIIC--KIS
hSmO	496	IGLPTKQPIPDCEIKNRPSLLVEKINLFAMFGTGIAMSTWVWTKATLLIW
rat.smo	500	IGLPTKKPIPDCEIKNRPSLLVEKINLFAMFGTGIAMSTWVWTKATLLIW
dros.smo	546	SVFEEK...SSCRIE NRPSVGVQLQLHLCLFSSGIVMSTWCWT PSSIETW
hSmO	546	RRTWCRLTGQSDDEPKRIKSKMKIAKAFSKRRHELQNPGQELSFSMHTVS
rat.smo	550	RRTWCRLTGHSDDEPKRIKSKMKIAKAFSKRRHELQNPGQELSFSMHTVS
dros.smo	593	KRIYIRKKCGKEVVEEVKMPKHKVIAQTWAKRKD-FEDKGR-LSITLYN-T
hSmO	596	HGPPVAGLAFDLNE...PSADVSSAWAQHVTKMVARR...GAILPQDI
rat.smo	600	HGPPVAGLAFELNE...PSADVSSAWAQHVTKMVARR...GAILPQDV
dros.smo	640	HTDPVGLNFDVNDLNSSETNDISSTWAAAYLPQCVKRRMALTGAATGNSS
hSmO	638	SVTPVATPVPPEEQANLWL...VEAEIS...PELQKRLG...
rat.smo	642	SVTPVATPVPPEEQANLWL...VEAEIS...PELEKRLG...
dros.smo	689	SHGPARKNSLDS EISVSVRRHVSVESRRNSVDSQVS VKIAEMKTKVASRRSG

FIG. 5C

19 / 24

FIG. 5D

FIG. 6A

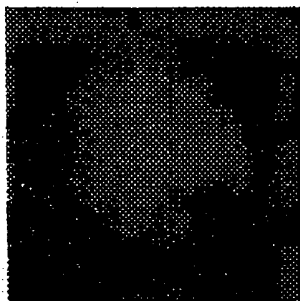


FIG. 6B



FIG. 6C



FIG. 6D

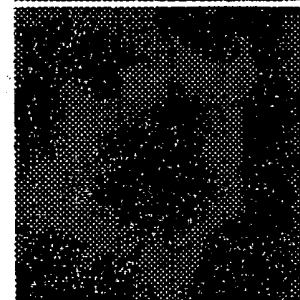


FIG. 6E

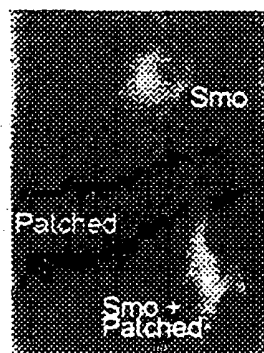
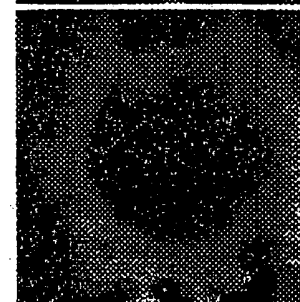


FIG. 7A

22 / 24

FIG. 6F

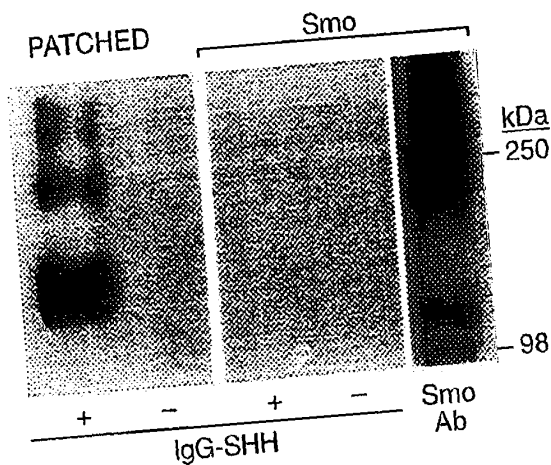


FIG. 6G

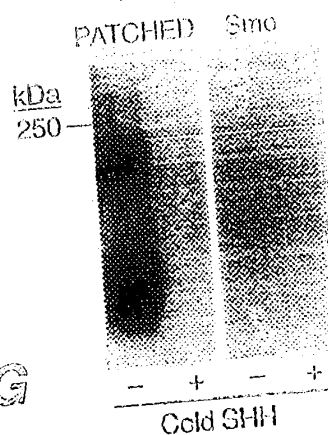
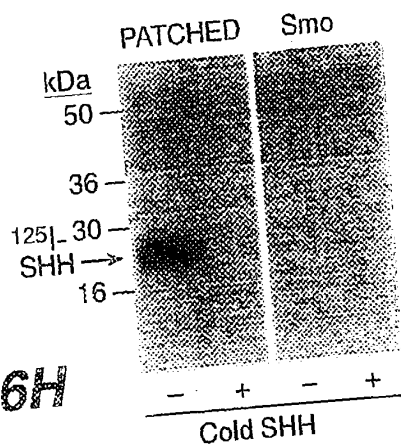
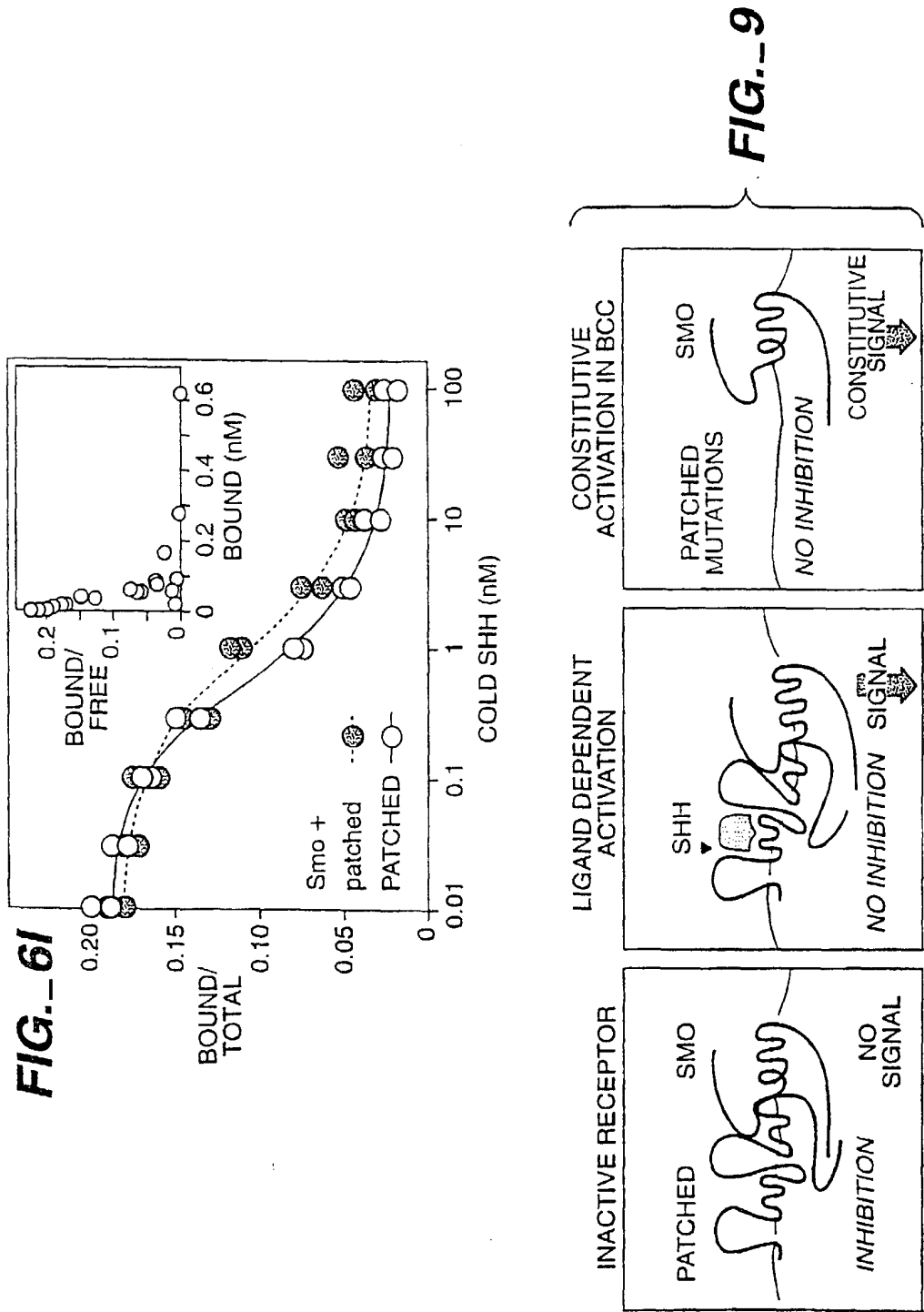


FIG. 6H





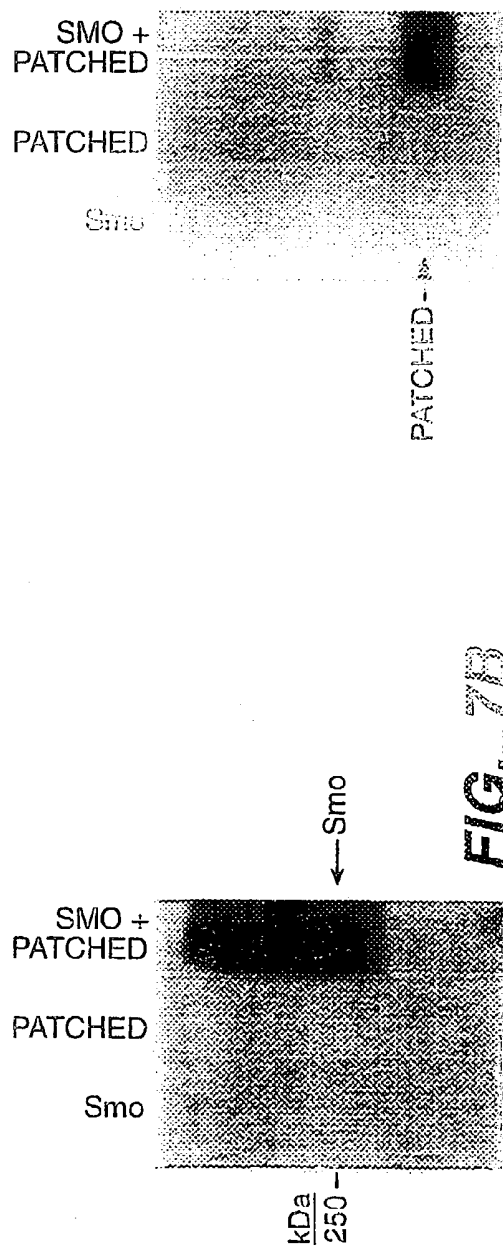


FIG. 7C

FIG. 7B

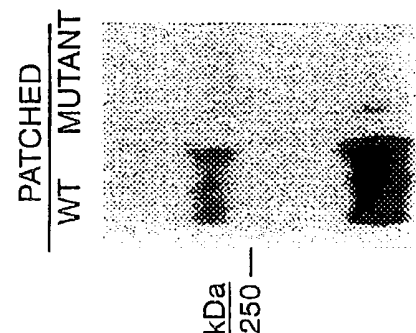


FIG. 8

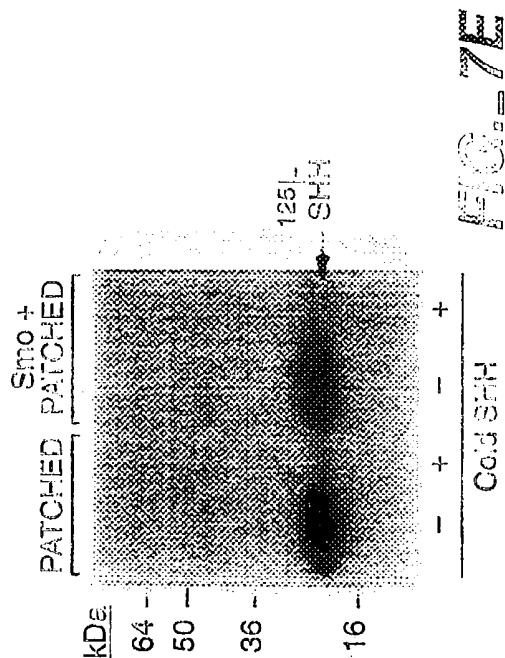


FIG. 7E

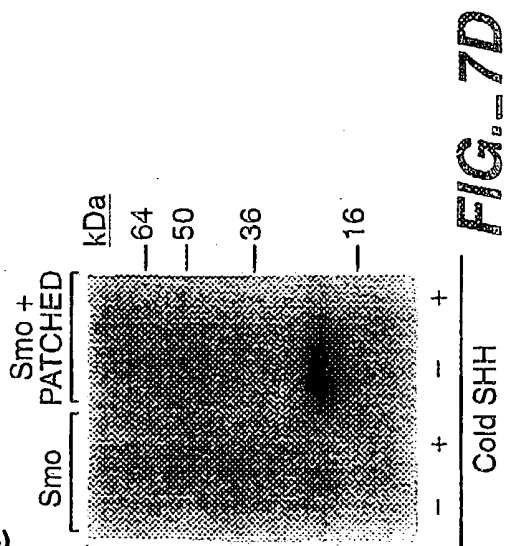


FIG. 7D

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 97/17433

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C07K14/47 C12N15/12

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	VAN DEN HEUVEL ET AL.: "Smoothened encodes a receptor- like serpentine protein required for hedgehog signalling" NATURE, vol. 382, 8 August 1996, pages 547-51, XP002054237 cited in the application	
P,X	D.M.STONE ET AL.: "The tumor suppressor gene patched encodes a candidate receptor for sonic hedgehog" NATURE, vol. 384, 14 November 1996, pages 129-134, XP002054238 see figure 1	1-32



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents :

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- "Z" document member of the same patent family

Date of the actual completion of the international search

2 February 1998

Date of mailing of the international search report

20.02.98

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